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OM protein - protein search, using sw model

Run on: December 15, 2003, 14:53:43 ; Search time 17 Seconds

(without alignments)

857.546 Million cell updates/sec

Title: US-09-831-805A-6

Perfect score: 310

Sequence: 1 MALRPPRLCARLPDFPL.....VNVRTDEEGDFRKSSFVI 310

Scoring table: OLIGO

GapOp 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters:

127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query | Match | Length | DB | ID | Description |
|------------|-------|-------|-------|--------|------------|--------|-------------------|
| 1 | 8 | 2.6 | 80 | 1 | TX2A_PHONI | P81793 | phoneutria |
| 2 | 8 | 2.6 | 342 | 1 | 1CXX_HUMAN | P10321 | homo sapien |
| 3 | 8 | 2.6 | 366 | 1 | 1C02_GORGO | P30385 | gorilla gorilla |
| 4 | 8 | 2.6 | 366 | 1 | 1C03_GORGO | P30386 | gorilla gorilla |
| 5 | 8 | 2.6 | 366 | 1 | 1C04_GORGO | P30387 | gorilla gorilla |
| 6 | 8 | 2.6 | 366 | 1 | 1C11_HUMAN | Q29631 | homo sapien |
| 7 | 8 | 2.6 | 435 | 1 | YGIK_SALTY | P40800 | salmonella |
| 8 | 7 | 2.3 | 161 | 1 | TATB_STRCO | Q9fbk8 | streptomyce |
| 9 | 7 | 2.3 | 224 | 1 | XLR1_MOUSE | Q9z114 | mus musculus |
| 10 | 7 | 2.3 | 244 | 1 | TNEC_HUMAN | Q06643 | homo sapien |
| 11 | 7 | 2.3 | 302 | 1 | HTPK_AQUAE | Q67798 | aquifex aeo |
| 12 | 7 | 2.3 | 306 | 1 | TNFC_MOUSE | P41155 | mus musculus |
| 13 | 7 | 2.3 | 310 | 1 | TNFC_MARMO | Q9jm10 | marmota monax |
| 14 | 7 | 2.3 | 333 | 1 | GPR8_HUMAN | P48146 | homo sapien |
| 15 | 7 | 2.3 | 343 | 1 | HMD_METVO | P00840 | methanococcus |
| 16 | 7 | 2.3 | 374 | 1 | TRM1_SULTO | Q971v9 | sulfolobus |
| 17 | 7 | 2.3 | 403 | 1 | TYRP_ECOLI | P18199 | escherichia |
| 18 | 7 | 2.3 | 417 | 1 | PVR_CERAE | P32506 | cercopithecus |
| 19 | 7 | 2.3 | 417 | 1 | PVR_HUMAN | P15151 | homo sapien |
| 20 | 7 | 2.3 | 454 | 1 | APY_SOLTU | P80595 | solanum tuberosum |
| 21 | 7 | 2.3 | 481 | 1 | LMB4_STRIN | P46104 | streptomyce |
| 22 | 7 | 2.3 | 491 | 1 | CPB4_RABIT | P00178 | oryctolagrus |
| 23 | 7 | 2.3 | 491 | 1 | CPBS_RABIT | P12789 | oryctolagrus |
| 24 | 7 | 2.3 | 524 | 1 | GTP2_HUMAN | P11168 | homo sapien |
| 25 | 7 | 2.3 | 574 | 1 | IRL2_MOUSE | Q9er87 | mus musculus |
| 26 | 7 | 2.3 | 595 | 1 | IF2P_ARCFU | P02490 | archaeoglobus |
| 27 | 7 | 2.3 | 617 | 1 | PYS1_PSEAE | O06583 | pseudomonas |
| 28 | 7 | 2.3 | 643 | 1 | S212_HUMAN | Q92959 | homo sapien |
| 29 | 7 | 2.3 | 643 | 1 | S212_MOUSE | Q9ep55 | mus musculus |
| 30 | 7 | 2.3 | 643 | 1 | S212_RAT | Q00910 | rattus norvegicus |
| 31 | 7 | 2.3 | 688 | 1 | PYS2_PSEAE | Q06584 | pseudomonas |
| 32 | 7 | 2.3 | 693 | 1 | NCP2_ASPNG | Q00141 | aspergillus galli |
| 33 | 7 | 2.3 | 697 | 1 | TGM2_CHICK | Q01841 | gallus gallus |

ALIGNMENTS

| Query Match | 2.6% | Score 8; | DB 1; | Length 342; |
|-----------------------|--|----------------|-------|-------------|
| Best Local Similarity | 10.00% | Pred. No. 4.7; | | |
| Matches | 8; | Conservative | 0; | Gaps 0 |
| PROTEIN ID | TX3A_PHONI | STANDARD; | PRT; | 80 AA. |
| AC | PP81753; | | | |
| TT | 28-FEB-2003 (Rel. 41, Created) | | | |
| DT | 28-FEB-2003 (Rel. 41, Last sequence update) | | | |
| DT | 28-FEB-2003 (Rel. 41, Last annotation update) | | | |
| DB | Neurotoxin Pn3A precursor. | | | |
| OS | Phoneutria nigriventer (Brazilian armed spider). | | | |
| OC | Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae; | | | |
| OC | Araenomorphae; Entelegynae; Lycosoidea; Ctenidae; Phoneutria. | | | |
| OX | NCBI_TaxID=6918; | | | |
| [1] | | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | TISSUE=Venom gland; | | | |
| RX | Medline=99053416; PubMed=9839681; | | | |
| RA | Kalapothakis E.; Penaforte C.J.; Leao R.M.; Cruz J.S.; Prado V.F., | | | |
| RA | Cordeiro M.N.; Diniz C.R.; Romano-Silva M.A.; Prado M.A.M., | | | |
| RA | Gomes M.V.; Beirão P.S.S.; | | | |
| RT | "Cloning, cDNA sequence analysis and patch clamp studies of a toxin from the venom of the armed spider (Phoneutria nigriventer)."; | | | |
| RT | Toxicon 36(1971-1980)(1998). | | | |
| CC | -- FUNCTION: Antagonist of L-type calcium channels (By similarity). | | | |
| CC | -- SUBCELLULAR LOCATION: Secreted. | | | |
| CC | -- TISSUE SPECIFICITY: Expressed by the venom gland. | | | |
| CC | -- SIMILARITY: BELONGS TO THE SPIDER TOXIN TX3 FAMILY. | | | |
| DR | InterPro: IPR004169; spider-toxin. | | | |
| PFam | PF02819; spider-toxin; 1. | | | |
| KW | Calcium channel inhibitor; Toxin; Neurotoxin; Ionic channel inhibitor; Signal. | | | |
| KW | POTENTIAL. | | | |
| FT | SIGNAL 1 21 BY SIMILARITY. | | | |
| FT | PROPEP 22 37 NEUROTOXIN PN3A. | | | |
| FT | CHAIN 38 71 BY SIMILARITY. | | | |
| FT | PROPEP 72 80 B5BF209257BB6793 CRC64; | | | |
| SQ | SEQUENCE 80 AA; 8937 MW; | | | |
| | 2.6% 82270.8 DB 1; Length 342; | | | |
| | Query Match 2.6%; Score 8; | | | |
| | Best Local Similarity 10.00%; Pred. No. 4.7; | | | |
| | Matches 8; Conservative 0; | | | |
| | Mismatches 0; Indels 0; | | | |
| | Gaps 0 | | | |

PIR; JH0545; JH0545.

DR HSSP; P30655; IgA1E.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003597; Ig-cl.

DR InterPro; IPR007110; Ig-cl.

DR InterPro; IPR003106; Ig_MHC.

DR InterPro; IPR001039; MHC_I.

Pfam; PF00047; Ig_1.

DR SMART; SM00429; MHC_I; 1.

DR PRINTS; PRO1638; MHCCLASSI.

DR PROSITE; PS50335; Ig_LIKE; 1.

DR PROSITE; PS50050; MHC_I; 1.

DR PROSITE; PS50047; IgCl; 1.

DR PROSITE; PS50835; Ig_LIKE; 1.

DR PROSITE; PS00290; Ig_MHC; FALSE_NEG.

MHC_I; Transmembrane; Glycoprotein; Signal.

SIGNAL 1 24 BY SIMILARITY.

FT CHAIN 25 366 CLASS I HISTOCOMPATIBILITY ANTIGEN,

FT DOMAIN 25 114 GOGO-C0201 ALPHA CHAIN.

FT DOMAIN 115 206 EXTRACELLULAR ALPHA-1.

FT DOMAIN 207 298 EXTRACELLULAR ALPHA-2.

FT DOMAIN 299 308 EXTRACELLULAR ALPHA-3.

CONNECTING PEPTIDE.

FT TRANSMEM 309 333 CYTOPLASMIC TAIL.

FT DOMAIN 334 366 BY SIMILARITY.

FT DISULFID 125 188 BY SIMILARITY.

FT DISULFID 227 283 BY SIMILARITY.

FT CARBOHYD 110 110 N-LINKED (GLCNAC. . .) (BY SIMILARITY).

SQ SEQUENCE 366 AA; 40954 MW; 05E159364C769FC5 CRC64;

Query Match 2.6%; Score 8; DB 1; Length 366;

Best Local Similarity 100.0%; Pred. No. 5;

Matches 8; Conservative 0; Mismatches 0; Gaps 0; Indels 0; Gaps 0;

Qy 249 VLVVLAVL 256

Db 317 VLVVLAVL 324

RESULT 5

1C04_GORGORGO STANDARD; PRT; 366 AA.

ID _1C04_GORGORGO P30387; AC P30387; (Rel. 25, Created)

DT 01-APR-1993 (Rel. 25, Last sequence update)

DT 01-APR-1993 (Rel. 25, Last annotation update)

DE Class I histocompatibility antigen, GOGO-C0203 alpha chain precursor.

OS Gorilla gorilla gorilla (Lowland gorilla)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.

OX NCBI_TaxID=9595;

RN [1] SEQUENCE FROM N.A.

RX MEDLINE=92078860; PubMed=1744581;

RA Lawlor D.A., Warren B., Taylor P., Parham P.; RT "Gorilla class I major histocompatibility complex alleles: comparison to human and chimpanzee class I."

RT "Gorilla class I major histocompatibility complex alleles: comparison to human and chimpanzee class I."

DB Class I histocompatibility antigen, GOGO-C0202 alpha chain precursor.

OS Gorilla gorilla gorilla (Lowland gorilla).

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.

OX NCBI_TaxID=9595;

RN [1] SEQUENCE FROM N.A.

RX MEDLINE=92078860; PubMed=1744581;

RA Lawlor D.A., Warren B., Taylor P., Parham P.; RT "Gorilla class I major histocompatibility complex alleles: comparison to human and chimpanzee class I."

RT "Gorilla class I major histocompatibility complex alleles: comparison to human and chimpanzee class I."

RL J. Exp. Med. 174:1491-1505 (1991).

-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.

-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).

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CC DR EMBL; X60248; CAA42800.1; -

CC DR PIR; JH0547; JH0547.

CC DR HSSP; P30685; IgAE.

CC DR InterPro; IPR007110; Ig-like.

CC DR InterPro; IPR0031597; Ig-cl.

CC DR InterPro; IPR003006; Ig_MHC.

CC DR InterPro; IPR001039; MHC_I.

RESULT 6
IC11_HUMAN

| ID | IC11_HUMAN | STANDARD; | PRT; | 366 AA. |
|-----------------------|---|-----------------------------------|------|---------|
| AC | Q29631; | | | |
| DT | 01-NOV-1997 | (Rel. 35, Created) | | |
| DT | 01-NOV-1997 | (Rel. 35, Last sequence update) | | |
| DT | 16-OCT-2001 | (Rel. 40, Last annotation update) | | |
| DE | HIA class I histocompatibility antigen, Cw-7 Cw*0704 alpha chain precursor. | | | |
| GN | HLA-C OR HLA-C. | | | |
| OS | Homo sapiens (Human). | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | | |
| OX | NCBI_TaxID=9606; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RX | MEDLINE=96086482; PubMed=7482492; | | | |
| RA | Vilches C., Bunce M., de Pablo R., Herrero M.J., Kreisler M.; | | | |
| RT | "Anchored PCR cloning of the novel HLA-Cw*0704 allele detected by PCR-SSP." | | | |
| RT | Tissue Antigens 46:19-23(1995). | | | |
| RN | [2] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | TISSUE-Blood; | | | |
| RX | MEDLINE=96232973; PubMed=8655351; | | | |
| RA | Wang H., Tokunaga K., Ishikawa Y., Asahina A., Kuwata S., Akaza T., Tadokoro K., Shibata Y., Takiguchi M., Juji T., | | | |
| RT | "Identification and DNA typing of two Cw alleles (Cw*0702 and Cw*0704) in Japanese, with the corrected sequence of Cw*0702." | | | |
| RJL | Hum. Immunol. 45:52-58 (1996). | | | |
| CC | -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM. | | | |
| CC | -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN). | | | |
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| CC | ----- | | | |
| CC | CC --> X83394; CAA58313.1; DR EMBL; X83394; CAA58313.1; DR EMBL; D4952; RAA08300.1; DR PIR; I37078; I37078. DR HSSP; P30460; IAGD. DR MIM; 142840; DR InterPro; IPR007110; Ig-like. DR InterPro; IPR003597; Ig_C1. DR InterPro; IPR003006; Ig_MHC. DR InterPro; IPR001039; MHC_I. DR Pfam; PF00047; Ig_1. DR Pfam; PF00129; MHC_I. DR PRINTS; PRO1638; MHCCLASSI. DR Prodrom; PD000050; MHC_I. DR SMART; SM00407; IgC1_1. DR PROSITE; PS05035; Ig_LIKE; 1. DR PROSITE; PS00230; Ig_MHC; FALSE NEG. DR MHC_I; Transmembrane; Glycoprotein; Signal. | | | |
| CC | FT SIGNAL 1 24 CLASS I HISTOCOMPATIBILITY ANTIGEN. FT CHAIN 25 366 GOGO-CO23 ALPHA CHAIN. | | | |
| FT | DOMAIN 25 114 EXTRACELLULAR ALPHA-1. | | | |
| FT | DOMAIN 115 206 EXTRACELLULAR ALPHA-2. | | | |
| FT | DOMAIN 207 298 EXTRACELLULAR ALPHA-3. | | | |
| FT | DOMAIN 299 308 CONNECTING PEPTIDE. | | | |
| FT | TRANSMEM 309 332 CYTOPLASMIC TAIL. | | | |
| FT | DOMAIN 333 366 BY SIMILARITY. | | | |
| FT | DISULFID 125 188 BY SIMILARITY. | | | |
| FT | DISULFID 227 283 BY SIMILARITY. | | | |
| FT | CARBOND 110 110 N-LINKED (GLCNAC. . .) (BY SIMILARITY). | | | |
| SQ | SEQUENCE 366 AA; 40970 MW; EB962C8189CAC001 CRC64; Cw-7 CW*0704 ALPHA CHAIN. | | | |
| Query Match | 2.6% Score 8; DB 1; Length 366; | | | |
| Best Local Similarity | 100.0%; Pred. No. 5; | | | |
| Matches | 8; Conservative 0; Mismatches 0; Gaps 0; | | | |
| Qy | 249 VLVVLAVL 256 | | | |
| Db | 317 VLVVLAVL 324 | | | |
| RESULT 7 | YGIK_SALTY | | | |
| YGIK_SALTY | STANDARD; | | | |
| AC | P40800; | | | |
| Matched | 25 | | | |
| Best Local Similarity | 100.0% | | | |
| Matches | 8; Conservative 0; Mismatches 0; Gaps 0; | | | |
| Qy | 249 VLVVLAVL 256 | | | |
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| Query Match | 2.6% Score 8; DB 1; Length 366; | | | |
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| Matches | 8; Conservative 0; Mismatches 0; Gaps 0; | | | |
| YGIK_SALTY | STANDARD; | | | |
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| Matched | 25 | | | |
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| Matches | 8; Conservative 0; Mismatches 0; Gaps 0; | | | |
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| AC | P40800; | | | |
| Matched | 25 | | | |
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| AC | P40800; | | | |
| Matched | 25 | | | |
| Best Local Similarity | 100.0% | | | |
| Matches | 8; Conservative 0; Mismatches 0; Gaps 0; | | | |
| Qy | 249 VLVVLAVL 256 | | | |
| Db | 317 VLVVLAVL 324 | | | |
| RESULT 7 | YGIK_SALTY | | | |
| YGIK_SALTY | STANDARD; | | | |
| AC | P40800; | | | |
| Matched | 25 | | | |
| Best Local Similarity | 100.0% | | | |
| Matches | 8; Conservative 0; Mismatches 0; Gaps 0; | | | |
| Qy | 249 VLVVLAVL 256 | | | |
| Db | 317 VLVVLAVL 324 | | | |
| RESULT 7 | YGIK_SALTY | | | |
| YGIK_SALTY | STANDARD; | | | |
| AC | P40800; | | | |
| Matched | 25 | | | |
| Best Local Similarity | 100.0% | | | |
| Matches | 8; Conservative 0; Mismatches 0; Gaps 0; | | | |
| Qy | 249 VLVVLAVL 256 | | | |
| Db | 317 VLVVLAVL 324 | | | |
| RESULT 7 | YGIK_SALTY | | | |
| YGIK_SALTY | STANDARD; | | | |
| AC | P40800; | | | |
| Matched | 25 | | | |
| Best Local Similarity | 100.0% | | | |
| Matches | 8; Conservative 0; Mismatches 0; Gaps 0; | | | |
| Qy | 249 VLVVLAVL 256 | | | |
| Db | 317 VLVVLAVL 324 | | | |
| RESULT 7 | YGIK_SALTY | | | |
| YGIK_SALTY | STANDARD; | | | |
| AC | P40800; | | | |
| Matched | 25 | | | |
| Best Local Similarity | 100.0% | | | |
| Matches | 8; Conservative 0; Mismatches 0; Gaps 0; | | | |
| Qy | 249 VLVVLAVL 256 | | | |
| Db | 317 VLVVLAVL 324 | | | |
| RESULT 7 | YGIK_SALTY | | | |
| YGIK_SALTY | STANDARD; | | | |
| AC | P40800; | | | |
| Matched | 25 | | | |
| Best Local Similarity | 100.0% | | | |
| Matches | 8; Conservative 0; Mismatches 0; Gaps 0; | | | |
| Qy | 249 VLVVLAVL 256 | | | |
| Db | 317 VLVVLAVL 324 | | | |
| RESULT 7 | YGIK_SALTY | | | |
| YGIK_SALTY | STANDARD; | | | |
| AC | P40800; | | | |
| Matched | 25 | | | |
| Best Local Similarity | 100.0% | | | |
| Matches | 8; Conservative 0; Mismatches 0; Gaps 0; | | | |
| Qy | 249 VLVVLAVL 256 | | | |
| Db | 317 VLVVLAVL 324 | | | |
| RESULT 7 | YGIK_SALTY | | | |
| YGIK_SALTY | STANDARD; | | | |
| AC | P40800; | | | |
| Matched | 25 | | | |
| Best Local Similarity | 100.0% | | | |
| Matches | 8; Conservative 0; Mismatches 0; Gaps 0; | | | |
| Qy | 249 VLVVLAVL 256 | | | |
| Db | 317 VLVVLAVL 324 | | | |
| RESULT 7 | YGIK_SALTY | | | |
| YGIK_SALTY | STANDARD; | | | |
| AC | P40800; | | | </ |

-!- SIMILARITY: BELONGS TO THE YIAN/YGIK FAMILY.

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CC bearing signal peptides with the twin arginine conserved motif S/T-R-R-X-F-L-K. This seq-independent pathway is termed TAT for twin arginine translocation system. This system mainly transports proteins with bound cofactors that require folding prior to export

CC -!- SUBCELLULAR LOCATION: Membrane bound (Probable).

CC -!- SIMILARITY: Belongs to the tatB family.

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CC EMBL; AL939122; CAC01351.1; -.

DR HAMAP; MF 00237; -1.

DR InterPro; IPR003998; TatB.

DR PRINTS; PRO1506; TATBPROTEIN.

KW Transport; Protein transport; Translocation; Transmembrane;

FT TRANSMEM 9 29 POTENTIAL.

FT TRANSMEM 57 77 POTENTIAL.

FT TRANSMEM 110 130 POTENTIAL.

FT TRANSMEM 146 166 POTENTIAL.

FT TRANSMEM 176 196 POTENTIAL.

FT TRANSMEM 226 246 POTENTIAL.

FT TRANSMEM 280 300 POTENTIAL.

FT TRANSMEM 321 341 POTENTIAL.

FT TRANSMEM 343 363 POTENTIAL.

FT TRANSMEM 367 387 POTENTIAL.

FT TRANSMEM 408 428 POTENTIAL.

FT CONFLICT 119 119 A -> R (IN REF. 1).

FT CONFLICT 124 124 A -> P (IN REF. 1).

SQ SEQUENCE 435 AA; 46004 MW; EEA19EFCFPE8A8A CRC64;

Query Match Score 2.6%; Score 8; DB 1; Length 435;

Best Local Similarity 100.0%; Pred. No. 5.8; Mismatches 0; Indels 0; Gaps 0;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 242 IGGIGGV 249

Db 236 IGGIGGV 243

RESULT 8

TATB_STRCO STANDARD; PRT; 161 AA.

AC Q9FBK6;

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DB sec-independent protein translocase protein tatB homolog.

GN TATB OR SC05150 OR SCP8.13.

OS Streptomyces coelicolor.

OC Bacteria; Actinobacteridae; Actinomycetales;

OC Streptomycineae; Streptomyctaceae; Streptomyces.

OX NCBI_TaxID=1902;

RN [1] SEQUENCE FROM N.A.

RC STRAIN=A3(2) / MI45;

RX MEDLINE=21996410; PubMed=12000953;

RA Bentley S.D., Chater K.F., Cerdeno-Taronga A.-M., Challis G.L., Thomson N.R., James K.D., Harris D.B., Quail M.A., Kieber H., Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M., Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kieser T., Larkie L., Murphy L., Oliver K., O'Neil S., Rabbitts E., Ratandream M.A., Rutherford K., Rutter S., Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K., Warren T., Wietzorek A., Woodward J., Barrell B.G., Parkhill J., Hopwood D.A.;

RT "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";

RT Nature 417:141-147(2002).

RL Gene 227:257-266(1999).

-!- FUNCTION: Required for correct localization of precursor proteins

CC -!- FUNCTION: MAY BE ACTIVE IN CELL ADHESION PROCESSES DURING RETINAL DEVELOPMENT BY SIMILARITY.

CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).

CC -!- TISSUE SPECIFICITY: Retinal-specific.

CC -!- SIMILARITY: Contains 1 F5/8 type C domain.

CC -----

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CC DR EMBL; AF084561; ADD21808_1; -.

DR EMBL; AF084567; ADD21809_1; -.

DR EMBL; AF084562; ADD21809_1; JOINED.

DR EMBL; AF084563; ADD21809_1; JOINED.

DR EMBL; AF084564; ADD21809_1; JOINED.

DR EMBL; AF084565; ADD21809_1; JOINED.

DR EMBL; AF084566; ADD21809_1; JOINED.

DR EMBL; AF084567; ADD21809_1; JOINED.

DR EMBL; AF084568; ADD21809_1; -.

DR EMBL; AF084569; ADD21809_1; ICST.

DR MGD; MGI:1336189; Rsi1h.

DR InterPro; IPR000421; FA58_C.

DR SMART; SM00231; FA58C_1; 1.

DR PROSITE; PS01285; FA8C_1; 1.

DR PROSITE; PS01286; FA8C_2; FALSE_NEG.

DR PROSITE; PS05022; FA8C_3; 1.

KW Cell adhesion; Signal.

FT SIGNAL_1 23 POTENTIAL.

FT CHAIN 24 224 X-LINKED JUVENILE RETINOSCHISIS PROTEIN.

FT DOMAIN 63 219 F5/8 TYPE C.

FT DISULFID 63 219 BY SIMILARITY.

FT SEQUENCE 224 AA; 25575 MW; 4536203CCC00E90E4 CRC64;

Query Match 2.3%; Score 7; DB 1; Length 224;

Best Local Similarity 100.0%; Pred. No. 32;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 FFLLLF 24

Ds 8 FFLLLF 14

RESULT 10

TNFC_HUMAN STANDARD; PRT; 244 AA.

ID TNFC_HUMAN ; STANDARD; PRT; 244 AA.

AC Q06643; P78370; Q99761;

DT 01-JUN-1994 (Rel. 29, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DB Lymphotoxin-beta (LT-beta) (Tumor necrosis factor C) (TNF-C) (Tumor necrosis factor ligand superfamily member 3).

DN LTB OR TNFSF3 OR TNFC.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OC NCBI_TaxID:9606;

RN [1] MEDLINE=93208881; PubMed=7916655;

RA Browning J.L., Ngam-Ek A., Lawton P., Demarinis J., Tizard R., Chow E.P., Hession C., O Brine-Greco B., Foley S.F., Ware C.F., RT "Lymphotoxin beta", a novel member of the TNF family that forms a heteromeric complex with lymphotoxin on the cell surface." Cell 72:847-856(1993).

RN [2] SEQUENCE FROM N.A. (ISOFORM 1 AND 2).

RP MEDLINE=97445965; PubMed=299492;

RX Warzocha K., Renard N., Charlot C., Bienvenu J., Coiffier B.,

DR InterPro; IPR001636; TNF_subf.
 DR Pfam; PF00229; TNF; 1.
 DR PRINTS; PR01234; TNBCROSISCT.
 DR ProDom; PDO02012; TNF_subf; 1.
 DR SMART; SM00207; TNF; 1.
 DR PROSITE; PS00251; TNF; 1.
 DR PROSITE; PS00449; TNF; 2; 1.
 KW Cytokine; Transmembrane; Glycoprotein; Signal-anchor;
 KW Alternative splicing; Polymorphism.
 FT DOMAIN 1 18 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 19 48 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 (POTENTIAL).
 FT DOMAIN 49 222 EXTRACELLULAR (POTENTIAL).
 FT CARBONYD 222 222 N-LINKED (GLCNAC...) (POTENTIAL).
 FT VARSPLIC 53 77 GLVTTETADPGAGAQGIGFQKLPEE -> GIGFRSQRSSQ
 KOISAPSGSQLPES (in isoform 2).
 FT VARSPLITC 78 244 /FTId=VSP_006441.
 FT VARIANT 70 70 Missing (In isoform 2).
 FT VARIANT 111 111 G -> E.
 FT CONFLICT 60 69 /FTId=VSP_006442.
 SQ .SEQUENCE 244 AA; 25390 MW; F41569459830EDAC CRC64;
 SQ .SEQUENCE 244 AA; 25390 MW; F41569459830EDAC CRC64;
 SQ .SEQUENCE 244 AA; 25390 MW; F41569459830EDAC CRC64;

Query Match Score 7; DB 1; Length 244;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 7; Conservative 0; Mismatches 0; Gaps 0;
 Qy 252 VLVAVL 258
 Db 40 VLVAVL 46

RESULT 11
 HTPX_AQUAE STANDARD PRT; 302 AA.
 ID HTPX_AQUAE
 AC 067796;
 DT 15-JUL-1999 (Rel. 3B, Created)
 DT 15-JUL-1999 (Rel. 3B, Last sequence update)
 DE Probable protease htpx homolog (EC 3.4.24.-).
 GN HTPX OR AQ_1991.
 OC Aquifex aeolicus.
 OC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
 NCBI_TaxID=63365;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HTPX,
 RX MEDLINE=98196666; PubMed=9833730;
 RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
 RA Graham D.E., Overbeek R., Sneed M.A., Kellar M., Aujay M., Huber R.,
 RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
 RT "The complete genome of the hyperthermophilic bacterium Aquifex
 aeolicus.";
 RL Nature 392:353-358 (1998).
 CC -I- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
 CC -I- SUBCELLULAR LOCATION: Integral membrane Protein (Potential).
 CC -I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M48

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 or send an email to license@isb-sib.ch).

CC EMBL; AE000766; AAC07747.1; -.
 DR PIR; B70471; B70471.
 DR MEROPS; M48.004; -.

DR HAMAP; MF_00198; -; 1.
 DR Interpro; IPR001915; Peptidase_M48.
 DR MTpeptidase.
 DR Prosite; PS00144; Peptidase_M48; 1.
 DR PROSITE; PS00144; ZINC_Protease; FALSE_NEG.
 KW Transmembrane; Hydrolase; Metalloprotease; Zinc; Complete proteome..
 FT TRANSMEM 27 47 POTENTIAL.
 FT TRANSMEM 151 171 POTENTIAL.
 FT TRANSMEM 195 215 POTENTIAL.
 FT METAL 141 141 ZINC (CATALYTIC) (BY SIMILARITY).
 FT ACT_SITE 142 142 BY SIMILARITY.
 FT METAL 145 145 ZINC (CATALYTIC) (BY SIMILARITY).
 SQ SEQUENCE 302 AA; 33030 MW; 322BBF481568895 CRC64;

Query Match Score 7; DB 1; Length 302;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 242 IGGIGDG 248
 Db 31 IGGIGDG 37

RESULT 12
 TNFC_MOUSE STANDARD PRT; 306 AA.
 ID TNFC_MOUSE
 AC P41155;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 RA Lymphtoxin-beta (LT-beta) (Tumor necrosis factor C) (TNF-C) (Tumor
 necrosis factor ligand superfamily member 3).
 RA LTB OR TNFSF3 OR TNFC.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10950;
 OX NCBI_TaxID=10950;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RX MEDLINE=93148600; PubMed=7846035;
 RA Pokholok D.K., Maroulakou I.G., Kuprash D.V., Alimzhanov M.B.,
 RA Kozlov S.V., Novobrantseva T.I., Turetskaya R.L., Green J.E.,
 RA Nedospasov S.A.;
 RA "Cloning and expression analysis of the murine lymphotoxin beta
 gene.";
 RT RL Proc. Natl. Acad. Sci. U.S.A. 92:674-678 (1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Spleen;
 RX MEDLINE=9308831; PubMed=7995544;
 RA Lawton P., Nelson J., Tizard R., Browning J.L.,
 RT RL "Characterization of the mouse lymphotoxin-beta gene.";
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Shaffier T., Ratcliffe A., Loretz C., Lasky S., Hood L.;
 RA "Sequence of the mouse major histocompatibility class III region."
 RA Submitted (OCT-1999) to the EMBL/GenBank/DDJ databases.
 CC -I- FUNCTION: Cytokine that binds to LTBR/TNFRSF3. May play a specific
 role in immune response regulation. Provides the membrane anchor
 for the attachment of the heterotrimeric complex to the cell
 surface.
 CC -I- SUBUNIT: Heterotrimer of either two LTB and one LTA subunits or
 CC (less prevalent) two LTA and one LTB subunits (By similarity).
 CC -I- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
 CC -I- SIMILARITY: Belongs to the tumor necrosis factor family.

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 or send an email to license@isb-sib.ch).

CC EMBL; AE000766; AAC07747.1; -.
 DR PIR; B70471; B70471.
 DR MEROPS; M48.004; -.

| SQ | SEQUENCE | 333 AA; | 36902 MW; | 23438B473FAF217BB CRC64; |
|------------------------------------|---|-----------------------|---|--------------------------|
| RA | Lehaeslahti M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D., | Query Match | 2.3%; | Score 7; DB 1; |
| RA | Marsh S.L., Martin S.L., McConnachie L.J., McMurtry A.A., | Best Local Similarity | 10.0%; | Pred. No. 45; |
| RA | Milne S.A., Mistriy D., Moore M.J.F., Mullikin J.C., Nickerson T., | Matches | 7; Conservative | 0; Mismatches |
| RA | Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I., | 0; Indels | 0; | Gaps |
| RA | Phillimore B.J.T., Prathalingam S.R., Plumb R.W., Ramsay H., | 0; | 0; | 0; |
| RA | Rice C.M., Ross M.T., Scott C.B., Sehra H.K., Shownkeen R., Sims S., | Qy | 249 VLVVLAV 255 | |
| RA | Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E., | | | |
| RA | Swann R.M., Sycamore N., Taylor R., Thomas D.W., Thorpe A., | | | |
| RA | Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M., | | | |
| RA | Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A., | | | |
| RA | Wilmng L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S., | | | |
| RA | Rogers J.; | | | |
| RT | "The DNA sequence and comparative analysis of human chromosome 20." | | | |
| RN | Nature 41:865-871(2001). | | | |
| [3] | VARIANT GLN-206. | RESULT 15 | | |
| RP | Zeng J., Liu M., Grau O., Capron A., Bahr G.M.; | RND_METVO | | |
| RT | "Identification of a novel amino acid substitution (R206Q) in the | ID | HMD_METVO | |
| RT | second extracellular loop of the opioid-somatostatin-like receptor | AC | Q50440; | |
| RT | Gene GPR8.; | DT | 01-NOV-1997 (Rel. 35, Created) | |
| Hum. | Mutat. 12:219-219(1998). | DT | 01-NOV-1997 (Rel. 35, Last sequence update) | |
| CC | -1- FUNCTION: ORPHAN RECEPTOR. COULD BIND AN OPIOD. | DT | 28-FEB-2003 (Rel. 41, Last annotation update) | |
| CC | -1- SUBCELLULAR LOCATION: Integral membrane protein. | DE | Coenzyme F420-dependent N(5),N(10)-methenyltetrahydromethanopterin | |
| CC | -1- TISSUE SPECIFICITY: FRONTEX, NOT IN CEREBELLUM. | DE | reductase (EC 1.5.99.11) (H(2)-forming N(5),N(10)- | |
| CC | HIPPOCAMPUS, HYPOTHALAMUS, PONS, PUTAMEN AND THALAMUS REGIONS. | DE | methylenetetrahydromethanopterin dehydrogenase) (H(2) -dependent | |
| CC | -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS. | DE | DE methylene-H(4)MPT dehydrogenase). | |
| CC | | GN | HMD. | |
| CC | | OS | Methanococcus voltae. | |
| CC | | OC | Archaea; Euryarchaeota; Methanococcaceae; Methanococcus; | |
| CC | | OC | NCBI_TAXID:2188; | |
| CC | | RN | [1] | |
| CC | | SEQUENCE FROM N.A. | | |
| CC | | RP | SEQUENCE FROM N.A. | |
| CC | | RC | SEQUENCE FROM DSM 1537 / PS; | |
| CC | | RA | Hartmann G.C.; Thauer R.K.; | |
| CC | | RL | Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases | |
| CC | | CC | -1- CATALYTIC ACTIVITY: N(5),N(10)-methylenetetrahydromethanopterin + | |
| CC | | CC | reduced coenzyme F420 = 5-methyl-5,6,7,8-tetrahydromethanopterin + | |
| CC | | CC | coenzyme F420. | |
| CC | | CC | -1- COFACTOR: ZINC (BY SIMILARITY). | |
| CC | | CC | -1- PATHWAY: Methanogenesis. | |
| CC | | CC | | |
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| CC | | | | |
| EMBL; U22492; AAC50198.1; -. | | | | |
| DR | EMBL; AL121581; CAC1004.1; -. | | | |
| PIR; I38974; I38974. | | | | |
| DR | Genev.; HGNC:4530; GPR8. | | | |
| MIN; 60731; -. | | | | |
| DR | GO; GO:0005887; C: integral to plasma membrane; TAS. | | | |
| DR | GO; GO:0004985; F:G-protein receptor activity; TAS. | | | |
| DR | GO; GO:0007186; P:G-protein coupled receptor protein signalin. . . TAS. | | | |
| DR | GO; GO:0007268; P:synaptic transmission; TAS. | | | |
| InterPro; IPR000276; GPCR_Rhodpsn. | | | | |
| Pfam; PF00001; 7tm_1. | | | | |
| PFAM; IPR004889; HMD. | | | | |
| DR | PROSITE; PS00237; GPCRRHODPSN. | | | |
| DR | PROSITE; PS00262; G-PROTEIN_RACEP_F1_1; 1. | | | |
| DR | G-Protein coupled receptor; Transmembrane; Glycoprotein; Lipoprotein; | | | |
| KW | Palmitate; Phosphorylation; Polymerism. | | | |
| DOMAIN | 1 45 | | | |
| TRANSMEM | 46 69 | | | |
| DOMAIN | 70 80 | | | |
| FT | TRANSMEM | 2 (POTENTIAL). | | |
| FT | DOMAIN | 105 105 | | |
| FT | TRANSMEM | 120 120 | | |
| FT | DOMAIN | 121 140 | | |
| FT | TRANSMEM | 141 165 | | |
| FT | DOMAIN | 166 185 | | |
| FT | TRANSMEM | 186 211 | | |
| FT | DOMAIN | 212 233 | | |
| FT | TRANSMEM | 234 257 | | |
| FT | DOMAIN | 258 282 | | |
| FT | TRANSMEM | 283 292 | | |
| FT | DOMAIN | 293 307 | | |
| FT | TRANSMEM | 308 333 | | |
| FT | DISULFID | 117 197 | | |
| FT | CARBONYD | 24 24 | | |
| FT | CARBONYD | 29 29 | | |
| FT | CARBONYD | 34 34 | | |
| FT | VARIANT | 206 206 | | |
| FT | | R -> Q. | | |
| FT | | T -> S (IN REF. 2). | | |
| CONFFLICT | 305 305 | | | |

OS Sulfolobus tokodaii.
 OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
 OC Sulfolobus
 OX NCBI_TAXID=111955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=JCM 10545 / 7;
 RX MEDLINE=21456156; PubMed=11572479;
 RA Kawarabayashi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M., Fukui S., Burland V.,
 RA Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S., Burland V.,
 RA Nagai Y., Nishizawa K., Otsuka R., Takamiya M., Kato Y., Mori H., Motomura K.,
 RA Yoshizawa T., Tanaka T., Kudooh Y., Yamazaki J., Kushiida N., Oguchi A.,
 RA Aoki K.-I., Masuda S., Yanagi M., Nishimura M., Yamagishi A.,
 RA Oshima T., Kikuchi H.;
 RT "Complete genome sequence of an aerobic thermoacidophilic
 RT Crenarchaeon, *Sulfolobus tokodaii* strain7.";
 RL Res. 8:123-14 (2001).
 CC :- FUNCITION: Dimethylates a single guanine residue at position 26 of
 CC a number of tRNAs using S-adenosyl-L-methionine as donor of the
 CC methyl groups (By similarity).
 CC :- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + tRNA = S-adenosyl-L-
 CC homocysteine + tRNA containing N(2)-methylguanine.
 CC :- SIMILARITY: BELONGS TO THE TRM1 FAMILY.
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 CC EMBL: AP000985; BAB6311..1; -.
 DR HAMAP; MF_00290; ; 1.
 DR InterPro; IPR002005; TRM.
 DR Pfam; PF020205; TRM; 1.
 KW Transferase; Methyltransferase; tRNA processing; Complete proteome.
 SQ SEQUENCE 374 AA; 43333 MW; 0B4E6E3C2420B15F CRC64;
 Query Match Score 7; DB 1; Length 374;
 Best Local Similarity 100.0%; Pred. No. 50;
 Matches 7; Conservative 0; Mismatches 0; Gaps 0;
 DE Tyrosine-specific transport protein (Tyrosine permease).
 DE TYRP OR B1907 OR SF1933.
 OS Escherichia coli, and
 OS Shigella flexneri.
 OBacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 RN NCBI_TAXID=562, 623;
 RP SEQUENCE FROM N.A.
 RC SPECIES=E.coli; STRAIN=K12 / MG1655;
 RX MEDLINE=97426617; PubMed=9278503;
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Perna N.T., Burland V.,
 RA Baba T., Fujita K., Hayashi K., Inada T.,
 RA Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T.,
 RA Isomo K., Kasai H., Kimura S., Kitakawa M., Kitagawa M.,
 RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
 RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshina T.,
 RA Saito N., Sampai G., Seii Y., Sivabundaram S., Tagami H.,
 RA Takeno J., Take moto K., Wada C., Yamamoto Y., Horiuchi T.;
 RT RT 460-kb DNA sequence of the Escherichia coli K12 Genome
 RT corresponding to the 40.1-50.0 min region on the linkage map.;
 RL DNA Res. 3:379-392 (1996).
 RN SEQUENCE FROM N.A.
 RC SPECIES=S.flexneri; STRAIN=301 / serotype 2a;
 RX MEDLINE=21234590; PubMed=12334590;
 RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
 RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
 RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
 RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
 RA Yu J.;
 RT RT sequence of *Shigella flexneri* 2a: insights into pathogenicity
 RT through comparison with genomes of *Escherichia coli* K12 and O157.;
 RL Nucleic Acids Res. 30:432-441 (2002).
 CC :- FUNCTION: INVOLVED IN TRANSPORTING TYROSINE ACROSS THE CYTOPLASMIC
 CC MEMBRANE.
 CC :- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.
 CC :- INDUCTION: REPRESSION BY TYROSINE AND INDUCED BY PHENYLALANINE
 CC UNDER THE CONTROL OF REGULATORY PROTEIN TYR.
 CC :- SIMILARITY: Belongs to the amino acid/polyamine transporter family
 CC II. Mr / tnab / tyrp permease subfamily.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL: AE000284; AAC74977.1; -.
 DR InterPro; IPR002422; AArel_Permease2.
 DR InterPro; IPR002091; AArel_Permease2.
 RC SPECIES=E.coli; STRAIN=K12 / MG1655;
 RX MEDLINE=89008121; PubMed=3049553;
 RA Wooley P.J., Pittard A.J.;
 RA "DNA sequence of the gene (tyrp) encoding the tyrosine-specific
 RT transport system of *Escherichia coli*";
 RL J. Bacteriol. 170:4946-4949 (1988).
 RN [2]
 RP REVISIONS.
 RC SPECIES=E.coli;

| | | | | | | | |
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| FT | TRANSMEM | 81 | 101 | POTENTIAL. | | DR | PIR; A44194; A44194. |
| FT | TRANSMEM | 122 | 142 | POTENTIAL. | | DR | PIR; B44194; B44194. |
| FT | TRANSMEM | 148 | 168 | POTENTIAL. | | DR | InterPro; IPR07110; Ig-like. |
| FT | TRANSMEM | 184 | 204 | POTENTIAL. | | DR | InterPro; IPR03006; Ig_MHC. |
| FT | TRANSMEM | 217 | 237 | POTENTIAL. | | DR | InterPro; IPR03596; Ig_v. |
| FT | TRANSMEM | 275 | 295 | POTENTIAL. | | DR | Pfam; PF00047; Ig_3. |
| FT | TRANSMEM | 308 | 328 | POTENTIAL. | | DR | SMART; SM00406; Ig_1. |
| FT | TRANSMEM | 332 | 352 | POTENTIAL. | | DR | PROSITE; PS5035; Ig_LIKE; 3. |
| FT | TRANSMEM | 376 | 396 | POTENTIAL. | | KW | Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal; |
| FT | CONFLICT | 131 | 135 | AGGVV -> RRVAVL (IN REF. 1). | | KW | Repeat; Alternative splicing. |
| FT | CONFLICT | 222 | 224 | SAI -> ECD (IN REF. 1). | | KW | POTENTIAL. |
| SQ | SEQUENCE | 403 AA; | 42819 MW; | 7BECAA8 3679796 CRC64; | | FT | FT SIGNAL 1 |
| Query Match | Best Local Similarity | 2.3% | Score 7; DB 1; | Length 403; | | FT | 20 POTENTIAL. |
| Matches 7; | Conservative | 100.0%; | Pred. No. 53; | | | FT | POLYVIRUS RECEPTOR. |
| Qy | 253 LAVLALI | 259 | 0; | Mismatches 0; | Gaps 0; | FT | EXTRACELLULAR (POTENTIAL). |
| Db | 344 LAVLALI | 350 | | | | FT | POTENTIAL. |
| RESULT 18 | PVR_CERAE | STANDARD; | PRT; | 417 AA. | | FT | CYTOLASMIC (POTENTIAL). |
| ID | P22566; | | | | | FT | IG-LIKE V-TYPE. |
| AC | P32566; | | | | | FT | IG-LIKE C2-TYPE 1. |
| DT | 01-OCT-1993 (Rel. 27, Created) | | | | | FT | IG-LIKE C2-TYPE 2. |
| DT | 01-OCT-1993 (Rel. 27, Last sequence update) | | | | | FT | BY SIMILARITY. |
| DT | 15-SEP-2003 (Rel. 42, Last annotation update) | | | | | FT | BY SIMILARITY. |
| DB | Poliovirus receptor precursor. | | | | | FT | MISSING (In Isoform Delta). |
| GN | PVR OR PVS. | | | | | FT | /FTID=VSP 002622. |
| OS | Cercopithecus aethiops (Green monkey) (Grivet). | | | | | FT | /FTID=VSP 002623. |
| OC | Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | | | FT | Missing (In Isoform Delta). |
| OC | Cercopithecidae; Cercopithecinae; Cercopithecus. | | | | | FT | |
| NCBI_TaxID=9534; | | | | | | FT | |
| RN [1] | SEQUENCE FROM N.A. (ISOFORMS ALPHA AND DELTA). | | | | | FT | |
| RP | TISSUE=Kidney; | | | | | FT | |
| RX | MEDLINE=91059651; PubMed=1331308; | | | | | FT | |
| RA | Koike S., Ise I., Seto Y., Yonekawa H., Gotoh O., Nomoto A.; | | | | | FT | |
| RT | "A second gene for the African green monkey poliovirus receptor that has no putative N-glycosylation site in the functional N-terminal immunoglobulin-like domain." | | | | | FT | |
| RT | RT immunoglobulin-like domain."; | | | | | FT | |
| J. Virol. 66:7059-7066 (1992). | | | | | | FT | |
| CC | -1- FUNCTION: NOT KNOWN. USED BY POLIOVIRUS TO BIND AND ENTER THE CELL. | | | | | FT | |
| CC | -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (ALPHA FORM); SECRETED (BETA AND GAMMA FORMS). | | | | | FT | |
| CC | -1- ALTERNATIVE PRODUCTS: | | | | | FT | |
| CC | Event-Alternative splicing; Named isoforms=4; | | | | | FT | |
| CC | Name=Alpha; | | | | | FT | |
| CC | IsoId=P32506-1; Sequence=Displayed; | | | | | FT | |
| CC | Name=Beta; | | | | | FT | |
| CC | IsoId=P32506-3; Sequence=Not described; | | | | | FT | |
| CC | Name=Gamma; | | | | | FT | |
| CC | IsoId=P32506-4; Sequence=Not described; | | | | | FT | |
| CC | Name=Delta; | | | | | FT | |
| CC | IsoId=P32506-2; Sequence=VSP 002622, VSP 002623; | | | | | FT | |
| CC | -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. | | | | | FT | |
| CC | -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain. | | | | | FT | |
| CC | -1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains. | | | | | FT | |
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| CC | ----- | | | | | FT | |
| CC | DR D12611; BAA2136.1; -; | | | | | FT | |
| CC | EMBL; D12612; BAA2137.1; -; | | | | | FT | |

"The poliovirus receptor protein is produced both as membrane-bound and secreted forms.";

EMBO J. 9;3217-3224(1990).

[4]

SEQUENCE FROM N.A.

Kodovianli V., Severin J., Ge Y., Grable L., Kvistad E., Gordon L., Shannon M., Brower A., Olsen A.S., Smith J.M.; "Sequence analysis of a 1Mb region in 19q13.2 containing a zinc finger gene cluster.";

RT gene cluster.";

Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.

RL MEDLINE=91239515; PubMed=1851992;

RP DOMAINS=;

RR MEDLINE=91239515; PubMed=1851992;

RT FUNCTION: NOT KNOWN. USED BY POLIOVIRUS TO BIND AND ENTER THE CELL.

CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (ALPHA AND DELTA FORMS); SECRETED (BETA AND GAMMA FORMS).

CC -!- ALTERNATIVE PRODUCTS; Event=Alternative splicing; Named isoforms=4;

CC Name=Alpha;

CC IsoId=P15151-1; Sequence=Displayed;

CC Name=Beta;

CC IsoId=P15151-2; Sequence=VSP_002617;

CC Name=Gamma;

CC IsoId=P15151-3; Sequence=VSP_002618, VSP_002619;

CC Name=Delta;

CC IsoId=P15151-4; Sequence=VSP_002620, VSP_002621;

CC -!- MISCELLANEOUS: THE V-TYPE DOMAIN IS NECESSARY AND SUFFICIENT FOR VIRUS BINDING AND UPTAKE.

CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.

CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.

CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.

CC -!- DATABASE: NAME=PROW; Note=CD Guide CD155 entry CD155.htm".

CC www="http://www.ncbi.nlm.nih.gov/prow/cd/cd155.htm".

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CC EMBL; M24407; AAA36461.1; -;

DR EMBL; M24406; AAA36462.1; -;

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DR EMBL; X64331; CAA45677.1; JOINED.

DR EMBL; X64332; CAA45678.1; JOINED.

DR EMBL; X64333; CAA45679.1; JOINED.

DR EMBL; X64334; CAA45680.1; JOINED.

DR EMBL; X64335; CAA45681.1; JOINED.

DR EMBL; X64336; CAA45682.1; JOINED.

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DR EMBL; X64338; CAA45684.1; JOINED.

DR EMBL; X64339; CAA45685.1; JOINED.

DR EMBL; X64340; CAA45686.1; JOINED.

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DR EMBL; X64342; CAA45688.1; JOINED.

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DR EMBL; X64346; CAA45692.1; JOINED.

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DR EMBL; X64348; CAA45694.1; JOINED.

DR EMBL; X64349; CAA45695.1; JOINED.

DR EMBL; X64350; CAA45696.1; JOINED.

DR EMBL; X64351; CAA45697.1; JOINED.

DR EMBL; X64352; CAA45698.1; JOINED.

DR EMBL; X64353; CAA45699.1; JOINED.

DR EMBL; X64354; CAA45700.1; JOINED.

DR EMBL; X64355; CAA45701.1; JOINED.

DR EMBL; X64356; CAA45702.1; JOINED.

DR EMBL; X64357; CAA45703.1; JOINED.

DR EMBL; X64358; CAA45704.1; JOINED.

DR EMBL; X64359; CAA45705.1; JOINED.

DR EMBL; X64360; CAA45706.1; JOINED.

DR EMBL; X64361; CAA45707.1; JOINED.

DR EMBL; X64362; CAA45708.1; JOINED.

DR EMBL; X64363; CAA45709.1; JOINED.

DR EMBL; X64364; CAA45710.1; JOINED.

DR EMBL; X64365; CAA45711.1; JOINED.

DR EMBL; X64366; CAA45712.1; JOINED.

DR EMBL; X64367; CAA45713.1; JOINED.

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DR EMBL; X64371; CAA45717.1; JOINED.

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DR EMBL; X64375; CAA45721.1; JOINED.

DR EMBL; X64376; CAA45722.1; JOINED.

DR EMBL; X64377; CAA45723.1; JOINED.

DR EMBL; X64378; CAA45724.1; JOINED.

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DR EMBL; X64386; CAA45732.1; JOINED.

DR EMBL; X64387; CAA45733.1; JOINED.

DR EMBL; X64388; CAA45734.1; JOINED.

DR EMBL; X64389; CAA45735.1; JOINED.

DR EMBL; X64390; CAA45736.1; JOINED.

DR EMBL; X64391; CAA45737.1; JOINED.

DR EMBL; X64392; CAA45738.1; JOINED.

DR EMBL; X64393; CAA45739.1; JOINED.

DR EMBL; X64394; CAA45740.1; JOINED.

DR EMBL; X64395; CAA45741.1; JOINED.

DR EMBL; X64396; CAA45742.1; JOINED.

DR EMBL; X64397; CAA45743.1; JOINED.

DR EMBL; X64398; CAA45744.1; JOINED.

DR EMBL; X64399; CAA45745.1; JOINED.

DR EMBL; X64400; CAA45746.1; JOINED.

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DR EMBL; X64402; CAA45748.1; JOINED.

DR EMBL; X64403; CAA45749.1; JOINED.

DR EMBL; X64404; CAA45750.1; JOINED.

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DR EMBL; X64409; CAA45755.1; JOINED.

DR EMBL; X64410; CAA45756.1; JOINED.

DR EMBL; X64411; CAA45757.1; JOINED.

DR EMBL; X64412; CAA45758.1; JOINED.

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DR EMBL; X64414; CAA45760.1; JOINED.

DR EMBL; X64415; CAA45761.1; JOINED.

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DR EMBL; X64420; CAA45766.1; JOINED.

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DR EMBL; X64426; CAA45772.1; JOINED.

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DR EMBL; X64431; CAA45777.1; JOINED.

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DR EMBL; X64433; CAA45779.1; JOINED.

DR EMBL; X64434; CAA45780.1; JOINED.

DR EMBL; X64435; CAA45781.1; JOINED.

DR EMBL; X64436; CAA45782.1; JOINED.

DR EMBL; X64437; CAA45783.1; JOINED.

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DR EMBL; X64441; CAA45787.1; JOINED.

DR EMBL; X64442; CAA45788.1; JOINED.

DR EMBL; X64443; CAA45789.1; JOINED.

DR EMBL; X64444; CAA45790.1; JOINED.

DR EMBL; X64445; CAA45791.1; JOINED.

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DR EMBL; X64451; CAA45797.1; JOINED.

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DR EMBL; X64453; CAA45799.1; JOINED.

DR EMBL; X64454; CAA45800.1; JOINED.

DR EMBL; X64455; CAA45801.1; JOINED.

DR EMBL; X64456; CAA45802.1; JOINED.

DR EMBL; X64457; CAA45803.1; JOINED.

DR EMBL; X64458; CAA45804.1; JOINED.

DR EMBL; X64459; CAA45805.1; JOINED.

DR EMBL; X64460; CAA45806.1; JOINED.

DR EMBL; X64461; CAA45807.1; JOINED.

DR EMBL; X64462; CAA45808.1; JOINED.

DR EMBL; X64463; CAA45809.1; JOINED.

DR EMBL; X64464; CAA45810.1; JOINED.

DR EMBL; X64465; CAA45811.1; JOINED.

DR EMBL; X64466; CAA45812.1; JOINED.

DR EMBL; X64467; CAA45813.1; JOINED.

DR EMBL; X64468; CAA45814.1; JOINED.

DR EMBL; X64469; CAA45815.1; JOINED.

DR EMBL; X64470; CAA45816.1; JOINED.

DR EMBL; X64471; CAA45817.1; JOINED.

DR EMBL; X64472; CAA45818.1; JOINED.

DR EMBL; X64473; CAA45819.1; JOINED.

DR EMBL; X64474; CAA45820.1; JOINED.

DR EMBL; X64475

CC EMBL; M20855; AAA31223.1; - .
DR EMBL; S78830; AAB35177.1; - .
DR PIR; S31278; S31278.
DR HSSP; P00179; ID16.
DR InterPro; IPR01128; Cytochrome_P450.
PFam; PF00067; P450; 1.
PRINTS; PR0385; P450.
PROSITE; PS00085; CYTOCHROME_P450; 1.
KW Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;
KW Micromsome; Endoplasmic reticulum; Phosphorylation (BY PKA) (BY SIMILARITY).
FT MOD RES 128 128 PHOSPHORYLATION (BY PKA) (BY SIMILARITY).
FT METAL 436 436 IRON (HEME AXIAL LIGAND).
SEQUENCE 491 AA; 55769 MW; ABE2B97888408DCP CRC64;

Query Match 2.3%; Score 7; DB 1; Length 491;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 20 LLLLFRG 26
Db 16 LLLLFRG 22

RESULT 24
GTR2_HUMAN STANDARD; PRT; 524 AA.
AC P11168;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DE Solute carrier family 2, facilitated glucose transporter, member 2
DE (Glucose transporter type 2, liver).
GN SLC2A2 OR GLUT2.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID:9606;
RN [1]
SEQUENCE FROM N.A., AND VARIANT LEU-68.
RC TISSUE-Kidney, and Liver;
RX MEDLINE=81289735; PubMed=139950;
RA Kumamoto H., Seino S., Imura H., Sieno Y., Eddy R.L., Fukushima Y.,
RA Byers M.G., Showe T.B., Bell G.I., and chromosomal localization of mRNA
RT "Sequence, tissue distribution, and chromosomal localization of mRNA
encoding a human glucose transporter-like protein.";
Proc. Natl. Acad. Sci. U.S.A. 85:5434-5438 (1988).
CC -!- FUNCTION: FACILITATIVE GLUCOSE TRANSPORTER. THIS ISOFORM LIKELY
CC MEDIATES THE BIDIRECTIONAL TRANSFER OF GLUCOSE ACROSS THE PLASMA
CC MEMBRANE OF HEPATOCYTES AND IS RESPONSIBLE FOR UPTAKE OF GLUCOSE
CC BY THE BETA CELLS, MAY COMprise PART OF THE GLUCOSE-SENSING
CC MECHANISM OF THE BETA CELL, MAY ALSO PARTICIPATE WITH THE
CC NA(+) GLUCOSE COTRANSPORTER IN THE TRANSCELLULAR TRANSPORT OF
CC GLUCOSE IN THE SMALL INTESTINE AND KIDNEY.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Liver, insulin-producing beta cell, small
CC -!- INTESTINE, and KIDNEY.
CC -!- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY. GLUCOSE
TRANSPORTER SUBFAMILY.

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or send an email to license@isb-sib.ch).

CC -!- DR EMBL; J03810; AAA59514.1; - .
DR PIR; A31318; A31318.
DR Gene; HGNC:11006; SLC2A2.
DR GK; P1168; -.
DR OC Mus musculus (Mouse).
DR OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
DR OC MM; 138160; - .

GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0005624; C:membrane fraction; TAS.
DR GO; GO:0005355; F:glucose transporter activity; TAS.
DR GO; GO:0015758; P:carbohydrate metabolism; TAS.
DR InterPro; IPR007114; MFS.
DR InterPro; IPR005828; Sub transporter.
DR InterPro; IPR005529; Sugr_transporter.
DR InterPro; IPR003663; Sugar_transp.
DR Pfam; PF00083; sugar_tr_1.
DR PRINTS; PRO0171; SUGRTtransp.
DR TIGRFAMS; TIGR00879; SP_1.
DR PROSITE; PS00216; SUGAR TRANSPORT 1; 1.
DR PROSITE; PS00117; SUGAR TRANSPORT_2; 1.
KW Transmembrane; Sugar transport; Transport; Glycoprotein;
KW Multigene family; Polymorphism.
FT DOMAIN 1 10 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 11 31 1 (POTENTIAL).
FT DOMAIN 32 98 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 99 119 2 (POTENTIAL).
FT DOMAIN 120 127 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 128 148 3 (POTENTIAL).
FT DOMAIN 149 158 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 159 179 4 (POTENTIAL).
FT DOMAIN 180 187 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 188 208 5 (POTENTIAL).
FT DOMAIN 209 217 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 218 238 6 (POTENTIAL).
FT DOMAIN 239 303 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 304 324 7 (POTENTIAL).
FT DOMAIN 325 338 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 339 359 8 (POTENTIAL).
FT DOMAIN 360 368 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 369 389 9 (POTENTIAL).
FT DOMAIN 390 400 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 401 421 10 (POTENTIAL).
FT DOMAIN 422 433 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 434 454 11 (POTENTIAL).
FT DOMAIN 455 461 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 462 482 12 (POTENTIAL).
FT DOMAIN 483 524 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 62 62 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 68 68 /FTID=VAR_007169.
P -> L.
V -> I (IN dbSNP:1800572).
/FTID=VAR_014718.
T -> I (IN dbSNP:5400).
/FTID=VAR_014719.
L -> V (IN dbSNP:5397).
/FTID=VAR_014720.
SQ SEQUENCE 524 AA; 57489 MW; D400577207EC083 CRC64;
Query Match 2.3%; Score 7; DB 1; Length 524;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 201 TGTLVFT 207
Db 7 TGTLVFT 13

RESULT 25
IRL2_MOUSE STANDARD; PRT; 574 AA.
ID IRL2_MOUSE
Q9ER57;
AC Q9ER57;
DT 28-SEP-2003 (Rel. 41, Created)
DT 28-SEP-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Interleukin 1 receptor-like 2 precursor (IL-1Rrp2).
GN IL1R2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

| | |
|---|-----------------|
| OX NCBI_TaxID=10090; | Qy 18 FFLLIF 24 |
| RN [1] SEQUENCE FROM N.A.; PubMed=10882729; | Db 12 FFLLIF 18 |
| RX MEDLINE=20059050; PubMed=10882729; | |
| RA Born T.L., Smith D.E., Garka K.E., Renshaw B.R., Bertles J.S., | |
| RA Sims J.E., | |
| RT "Identification and characterization of two members of a novel class of the interleukin-1 receptor (IL-1R) family. Delineation of a new class of IL-1R-related proteins based on signaling."; | |
| RT J. Biol. Chem. 275:29946-29954 (2000). | |
| -!- FUNCTION: Receptor for interleukin 1 family member 9 (IL1F9). | |
| CC Binding to the agonist leads to the activation of NF- κ B (By similarity). | |
| CC -!- SUBCELLULAR LOCATION: Type I membrane protein. | |
| CC -!- MISCELLANEOUS: Does not bind interleukin 1 alpha (IL-1A) or interleukin 1 beta (IL-1B) (By similarity). | |
| CC -!- SIMILARITY: BELONGS TO THE INTERLEUKIN-1 RECEPTOR FAMILY. | |
| CC -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains. | |
| CC -!- SIMILARITY: Contains 1 TIR domain. | |
| CC -!- This SWISS-PROT entry is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch). | |
| CC EMBL; PF28433; AAG21367_1; -. | |
| DR HSSP; PI4778; LIRA. | |
| DR MGI; MGI:1913107; IL1rl2. | |
| DR InterPro; IPR003599; Ig. | |
| DR InterPro; IPR003006; Ig_NHC. | |
| DR InterPro; IPR007110; IL1_receptor1. | |
| DR InterPro; IPR004074; IL1 receptor/II. | |
| DR InterPro; IPR004076; IL1R_receptor. | |
| DR InterPro; IPR000157; TIR_domain. | |
| PFam; PF00047; Ig_3. | |
| PFam; PF01582; TIR; 1. | |
| DR SMART; SM00409; Ig; 2. | |
| SMART; SM00255; TIR; 1. | |
| DR PROSITE; PSS00835; Ig_LIKE; 2. | |
| DR PROSITE; PS00104; TIR; 1. | |
| KW Immunoglobulin domain; Transmembrane; Glycoprotein; Receptor; Signal; Repeat; Signal. | |
| FT CHAIN 1 21 | |
| FT DOMAIN 22 574 | |
| FT TRANSMEM 22 338 | |
| FT DOMAIN 360 574 | |
| FT DOMAIN 25 113 | |
| FT DOMAIN 132 215 | |
| FT DOMAIN 225 321 | |
| FT DOMAIN 384 542 | |
| FT DOMAIN 44 97 | |
| FT DISULFID 149 199 | |
| FT DISULFID 252 319 | |
| FT CARBOHYD 43 43 | |
| FT CARBOHYD 55 55 | |
| FT CARBOHYD 111 111 | |
| FT CARBOHYD 231 231 | |
| FT CARBOHYD 237 237 | |
| FT CARBOHYD 253 253 | |
| FT CARBOHYD 269 269 | |
| FT CARBOHYD 290 290 | |
| FT CARBOHYD 302 302 | |
| SEQUENCE 574 AA; 65108 MW; A677A7BBFA50A76 CRC64; | |
| Query Match 2.3%; Score 7; DB 1; Length 574; | |
| Best Local Similarity 100.0%; Pred. No. 72; | |
| Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | |
| Qy 18 FFLLIF 24 | |
| Db 12 FFLLIF 18 | |
| RESULT 26 | |
| IP2P_ARCFU STANDARD; PRT; 595 AA. | |
| ID IP2P_ARCFU AC O2950; DT 15-DEC-1998 (Rel. 37, Created) | |
| AC O2950; DT 15-DEC-1998 (Rel. 37, Last sequence update) | |
| DT 28-DEC-2003 (Rel. 41, Last annotation update) | |
| DE Probable translation initiation factor IF-2. | |
| GN OS Archaeoglobus fulgidus. | |
| OC Archaea; Euryarchaeota; Archaeoglobales; | |
| OC Archaeoglobus; Archaeoglobus. | |
| NCBI_TaxID=2234; OX RN [1] | |
| RP SEQUENCE FROM N.A. | |
| RC STRAIN=VC-16 / DSM 4304 / ATCC 49558; | |
| MDLINE=9804943; PubMed=9389475; | |
| RA Klein R.A., Clayton R.A., Tomb J.-F., White O., Nelson K.B., Kletch K.A., Dodson R.J., Hickey E.K., Peterson J.D., Richardson D.L., Kerlavage A.R., Graham D.E., Kyprides N.C., Fleischmann R.D., Quackenbush J., Lee N.H., Adams M.D., Loftus B., Peterson S., Peich C.I., McNeil L.K., Badger J.H., Giedke A., Zhou L., Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T., Cottrell M.D., Spriggs T., Artlach P., Kaine B.P., Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R., Venter J.C./ | |
| RA "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus." | |
| RT RT reducing archaeon Archaeoglobus fulgidus."; | |
| RL Nature 396:364-370 (1997). | |
| CC -!- FUNCTION: FUNCTION IN GENERAL TRANSLATION INITIATION BY PROMOTING THE BINDING OF THE FORMYLMETHIONINE-TRNA TO RIBOSOMES. SEEKS TO FUNCTION ALONG WITH EIF-2 (BY SIMILARITY). | |
| CC -!- SIMILARITY: BELONGS TO THE IF-2 FAMILY. | |
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| CC -!- SIMILARITY: BELOWS TO THE IF-2 FAMILY. | |
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| CC -!- DR EMBL; AE001051; AAB90465_1; -. | |
| CC -!- DR PIR; H69345; H69345. | |
| CC -!- DR TIGR; AF0768; | |
| CC -!- DR HAMAP; MF_00100; -; 1. | |
| CC -!- DR InterPro; IPR000795; EF_GTPbind. | |
| CC -!- DR InterPro; IPR004161; EIFTU_D2. | |
| CC -!- DR InterPro; IPR001778; IFP_1. | |
| CC -!- DR InterPro; IPR005225; SmalI_GRP. | |
| CC -!- DR InterPro; IPR004544; TIFP_aIF2. | |
| CC -!- DR Pfam; PF0009; GTP_BFTU_-1. | |
| CC -!- DR Pfam; PF03144; GTP_BFTU_D2; 1. | |
| CC -!- DR PRINTS; PR00315; ELONGAN_NFCFT. | |
| CC -!- DR Prodrom; PD186100; IFP; 1. | |
| CC -!- DR TIGRFAMS; TIGR00491; aIFP-2; 1. | |
| CC -!- DR TIGRFAMS; TIGR00231; small_GTP; 1. | |
| CC -!- DR PROSITE; PS01176; IFP; PAUSE_NEG. | |
| CC -!- KW Initiation factor; Protein biosynthesis; GTP-binding; Complete proteome. | |
| FT NP_BIND 20 27 GTP (BY SIMILARITY). | |
| FT NP_BIND 81 85 GTP (BY SIMILARITY). | |
| FT SEQUENCE 135 138 GTP (BY SIMILARITY). | |
| FT SEQUENCE 595 AA; 66680 MW; AFBD672E7D0D703 CRC64; Query Match 2.3%; Score 7; DB 1; Length 595; | |

| | | | | | |
|----|-----|--------------|--|--|--|
| Qy | 294 | IRTDDEGS 300 | | Best Local Similarity 100.0%; Pred. No. 74; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | 15-DEC-1998 (Rel. 37, Created) |
| Db | 353 | IRTDDEEG 359 | | | 15-DEC-1998 (Rel. 37, Last sequence update) |
| | | | | | 28-PEB-2003 (Rel. 41, Last annotation update) |
| | | | | | DT Solute carrier family 21 member 2 (Prostaglandin transporter) (PGT). |
| | | | | | DE SLC21A2. |
| | | | | | GN Homo sapiens (Human) |
| | | | | | OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Homino. |
| | | | | | OC NCBI TaxID=9606; |
| | | | | | OX NCBI_TaxID=9606; |
| | | | | | RN [1] |
| | | | | | RP SEQUENCE FROM N.A. |
| | | | | | RX MEDLINE=96379664; PubMed=8787677; |
| | | | | | RA Lu R.; Kanai N.; Bao Y.; Schuster V.L.; |
| | | | | | RT "Cloning, <i>in vitro</i> expression, and tissue distribution of a human prostaglandin transporter cDNA (hPGT)." ; |
| | | | | | RT J. Clin. Invest. 98:1142-1149(1996). |
| | | | | | RN [2] |
| | | | | | RP SEQUENCE FROM N.A. |
| | | | | | RX MEDLINE=98289812; PubMed=9618293; |
| | | | | | RA Lu R.; Schuster V.L.; |
| | | | | | RT "Molecular cloning of the gene for the human prostaglandin transporter hPGT; gene organization, promoter activity, and chromosomal localization." ; |
| | | | | | RL Biochem. Biophys. Res. Commun. 246:805-812(1998). |
| | | | | | CC -!- FUNCTION: May mediate the release of newly synthesized prostaglandins from cells, the transepithelial transport of prostaglandins, and the clearance of prostaglandins from the circulation. Transports PGD2, as well as PGEl, PGE2 and PGF2A. |
| | | | | | CC -!- SUBCELLULAR LOCATION: Intrigual membrane protein. |
| | | | | | CC -!- TISSUE SPECIFICITY: Ubiquitous. |
| | | | | | CC -!- SIMILARITY: BELONGS TO THE SLC21 FAMILY OF TRANSPORTERS. |
| | | | | | This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch). |
| | | | | | CC -!- EMBL; U70867; AAC09469.1; DR EMBL; AF056732; AAC62004.1; DR EMBL; AF056719; AAC62004.1; JOINED. CC -!- EMBL; AF056720; AAC62004.1; JOINED. EMBL; AF056721; AAC62004.1; JOINED. |
| | | | | | CC -!- EMBL; AF056722; AAC62004.1; JOINED. DR EMBL; AF056722; AAC62004.1; JOINED. DR EMBL; AF056723; AAC62004.1; JOINED. DR EMBL; AF056724; AAC62004.1; JOINED. DR EMBL; AF056725; AAC62004.1; JOINED. DR EMBL; AF056726; AAC62004.1; JOINED. DR EMBL; AF056727; AAC62004.1; JOINED. DR EMBL; AF056728; AAC62004.1; JOINED. DR EMBL; AF056729; AAC62004.1; JOINED. DR EMBL; AF056730; AAC62004.1; JOINED. DR EMBL; AF056731; AAC62004.1; JOINED. DR Genew; HGNC:10955; SLC21A2. DR MIM: 601460; DR GO; GO:0005887; C:integral to plasma membrane; TAS. DR GO; GO:0005624; C:membrane fraction; TAS. DR GO; GO:0005319; C:lipid transporter activity; TAS. DR GO; GO:0006869; P:lipid transport; TAS. DR InterPro; IPR04157; OATP_Cterm. DR InterPro; IPR04156; OATP_Nterm. |
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 FT TRANSMEM 366 386 POTENTIAL.
 FT TRANSMEM 400 420 POTENTIAL.
 FT TRANSMEM 511 531 POTENTIAL.
 FT TRANSMEM 551 571 POTENTIAL.
 FT TRANSMEM 606 626 N-LINKED (GLCNAC. .) (POTENTIAL).
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 Qy 28 LIGAVNL 34
 Db 367 LIGAVNL 373

RESULT 29
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 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
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 GN Mus musculus (Mouse)
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 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Murinae; Muridae;
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 [1] SEQUENCE FROM N.A. (ISOFORM 1), AND MUTAGENESIS OF VAL-610 AND
 ILE-611.
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 Pucci M.L., Bao Y., Chan B., Itoh S., Lu R., Copeland N.G.,
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 "Cloning of mouse prostaglandin transporter PGT cDNA: species-specific
 substrate affinities.";
 [2] SEQUENCE FROM N.A. (ISOFORM 2).
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 Klausner R.D., Collins F.S., Wagner L., Shevchenko A., Schulter G.D.,
 Altschul I.S.P., Zeisberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
 Hsiao F.,
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
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 Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 Blakesley R.W., Young A.C., Shevchenko Y., Bouffard G.G.,
 Rodriguez A.C., Grinwood E.D., Dickson M.C.,
 Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 Schnarch A., Schein J.E., Jones S.J.M., Marra M.A.,
 "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences."
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

-!- FUNCTION: May mediate the release of newly synthesized
 prostaglandins from cells, the transcellular transport of
 prostaglandins, and the clearance of prostaglandins from the
 circulation. Transports PGD2, as well as PGEl, PG2A,
 -!- SUBCELLULAR LOCATION: Integral membrane protein.
 -!- ALTERNATIVE PRODUCTS:

Event=Alternative splicing; Named isoforms=2;
 Name=-;
 IsoId=Q9EP15-1; Sequence=Displayed;
 Name=2;
 IsoId=Q9EP15-2; Sequence=VSP 006128, VSP 006129;
 Note-No experimental confirmation available;
 -!- TISSUE SPECIFICITY: Highly expressed in lung and liver. Detected
 at lower levels in kidney and skeletal muscle.
 -!- SIMILARITY: BELONGS TO THE SLC21 FAMILY OF TRANSPORTERS.

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CC DR EMBL; AF23958; AAC40332.1; -;
 CC DR EMBL; BC035200; AAH35200.1; -;
 CC DR MGD; MGI:13446021; Slc21a2;
 CC DR GO; GO:0015132; P:prostaglandin transport; IDA.
 CC DR InterPro; IPR007114; MFS.
 CC DR InterPro; IPR004157; OATP_Cterm.
 CC DR InterPro; IPR004156; OATP_Nterm.
 CC DR Pfam; PF0137; OATP_C_1.
 CC DR TIGRfams; TIGR0805; oat; 1.
 CC KW Transmembrane; Transport; Glycoprotein; Alternative splicing.
 CC FT TRANSMEM 31 51 POTENTIAL.
 CC FT TRANSMEM 31 51 POTENTIAL.
 CC FT TRANSMEM 72 92 POTENTIAL.
 CC FT TRANSMEM 101 121 POTENTIAL.
 CC FT TRANSMEM 172 192 POTENTIAL.
 CC FT TRANSMEM 210 230 POTENTIAL.
 CC FT TRANSMEM 258 278 POTENTIAL.
 CC FT TRANSMEM 321 341 POTENTIAL.
 CC FT TRANSMEM 365 385 POTENTIAL.
 CC FT TRANSMEM 399 419 POTENTIAL.
 CC FT TRANSMEM 510 530 POTENTIAL.
 CC FT TRANSMEM 550 570 POTENTIAL.
 CC FT TRANSMEM 605 625 POTENTIAL.
 CC FT CARBOHYD 134 134 (GLCNAC. .) (POTENTIAL).
 CC FT CARBOHYD 477 477 (GLCNAC. .) (POTENTIAL).
 CC FT CARBOHYD 490 490 (GLCNAC. .) (POTENTIAL).
 CC FT CARBOHYD 638 638 (GLCNAC. .) (POTENTIAL).
 CC FT VARSPLIC 368 368 GAVNPAAALGMLKREVFLQIPIVAATIMTISI
 ILCAPL -> AHQVYTRSLPPAAGTACAOLPSSTSLSAETM
 ESSTPSPMLAAST (in isoform 2).
 /FTID=VSP 006128.
 Missing (in isoform 2).
 /FTID=ISP 001129.
 V->M: NO EFFECT.
 I->G: NO EFFECT.
 L -> F (IN REF 1).
 SQ SEQUENCE 643 AA; 70146 MW; AC487386F847D9D8 CRC64;
 Query Match 2.3%; Score 7; DB 1; Length 643;
 Best Local Similarity 100.0%; Pred. No. 79;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0

RESULT 30
 S212 RAT STANDARD; PRT; 643 AA.
 ID S212 RAT
 AC 00910;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotator update)
 DT Solvate Carrier Family 2A member 2 Prostaglandin transporter (PGT)

DE (Matrin F/G).
 GN SLC21A2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_Taxid=10115;
 OX RN [1] -
 RP SEQUENCE FROM N.A.
 RC TISSUE-Liver;
 RX MEDLINE=91296785; PubMed=2068100;
 RA Hakes D.J., Bereznay R.;
 RT "Molecular cloning of matrin F/G: A DNA binding protein of the nuclear
 matrix that contains putative zinc finger motifs";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:6186-6190(1991).
 [2]
 CHARACTERS
 RX MEDLINE=95273959; PubMed=754369;
 RA Kanai N., Lu R., Satriano J.A., Bao Y., Wolkoff A.W., Schuster V.L.;
 RT "Identification and characterization of a prostaglandin transporter";
 RL Science 268:866-869(1995).
 CC I-- FUNCTION: May mediate the release of newly synthesized
 prostaglandins from cells, the transsepithelial transport of
 prostaglandins, and the clearance of prostaglandins from the
 circulation. Transports PGD2, as well as PGE1, PGF2 and PGF2A.
 CC II-- SUBCELLULAR LOCATION: Integral membrane protein.
 CC I-- SIMILARITY: BELONGS TO THE SLC21 FAMILY OF TRANSPORTERS.
 CC I-- CAUTION: Was originally (Ref.1) thought to be a nuclear DNA-
 binding protein.
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 DR EMBL; M64862; AAA41574.1; ALT_INIT.
 DR PIR; A41120; A41120.
 DR InterPro; IPR004157; OATP_Cterm.
 DR Pfam; PF03137; OATP_Nterm.
 DR PIGRFAM; TIGR009805; oat; 1.
 KW Transmembrane; Transport; Glycoprotein.
 FT TRANSMEM 27 47 POTENTIAL.
 FT TRANSMEM 71 91 POTENTIAL.
 FT TRANSMEM 101 121 POTENTIAL.
 FT TRANSMEM 172 192 POTENTIAL.
 FT TRANSMEM 210 230 POTENTIAL.
 FT TRANSMEM 258 278 POTENTIAL.
 FT TRANSMEM 321 341 POTENTIAL.
 FT TRANSMEM 365 385 POTENTIAL.
 FT TRANSMEM 399 419 POTENTIAL.
 FT TRANSMEM 512 532 POTENTIAL.
 FT TRANSMEM 550 570 POTENTIAL.
 FT TRANSMEM 605 625 POTENTIAL.
 FT TRANSMEM 134 134 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 478 478 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 491 491 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 638 638 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 643 AA; 70569 MW; A5699FB6C556PF58 CRC64;

2.3%; Score 7; DB 1; Length 643;
 Best Local Similarity 100.0%; Pred. No. 79;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PRT; 688 AA.
 PY52_PSEAE STANDARD; PRT; 688 AA.
 ID PY52_PSEAE AC Q06594;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pyocin S2 (EC 3.1. . .) (Killer protein).
 GN PY52 OR PA1150.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=287;
 RN [1] SEQUENCE FROM N.A., AND SEQUENCE OF 1-17.
 RP RP STRAIN=PAC; SEQUENCE FROM N.A., AND SEQUENCE OF 1-17.
 RC RX MEDIINE=9125934; PubMed=8491711;
 RA Sano Y., Matsui H., Kobayashi M., Kageyama M.;
 RT "Molecular structures and functions of pyocins S1 and S2 in
 Pseudomonas aeruginosa";
 RL J. Bacteriol. 175:2907-2916(1993).
 [2]
 RN RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 15692 / PAO1;
 RX MEDLINE=20437337; PubMed=10984043;
 RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
 Brinkman F.S.L., Hufnagle W.O., Kowalchuk D.J., Lagrou M.,
 Hickey M.J., Tolentino E., Westbroek-Wadman S., Yuan Y.,
 Coltrry L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
 Brody L.L., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 Reizer J., Salter M.H., Hancock R.E.W., Lory S., Olson M.V.;
 RA "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
 opportunistic pathogen";
 RT Nature 405:959-964(2000).
 CC I-- FUNCTION: CAUSES BREAKDOWN OF CHROMOSOMAL DNA AS WELL AS COMPLETE
 INHIBITION OF LIPID SYNTHESIS IN SENSITIVE CELLS.
 CC I-- SUBUNIT: PURIFIED PYOCIN S2 MAKES UP A COMPLEX OF THE TWO (LARGE
 AND SMALL) PROTEINS: THE LARGE PROTEIN, BUT NOT THE PYOCIN
 COMPLEX, SHOWS IN VITRO DNASE ACTIVITY.
 CC I-- MISCELLANEOUS: PYOCINS CONTAIN N-TERMINAL RECEPTOR-BINDING DOMAIN,
 TRANSLOCATION DOMAIN AND C-TERMINAL DNASE DOMAIN.
 CC I-- SIMILARITY: BELONGS TO THE NUCLEASE FAMILY OF COLICINS AND
 PYOSINS.
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 CC DR EMBL; D12708; BAA0203.1; -.
 CC DR EMBL; AE004545; AAG04539.1; -.
 CC DR PIR; C36907; C36907.
 CC DR PIR; D83501; D83501.
 CC DR HSSP; Q4711; TCBI.
 CC DR InterPro; IPR002711; HNNH.
 CC DR InterPro; IPR003615; HNNH nuc.
 CC DR InterPro; IPR003060; Pyocin_killer.
 CC DR Pfam; PF01844; HNNH.1.
 CC DR PRINTS; PR01300; PYOCINKILLER.
 CC DR SMART; SM00507; HNNHC.1.
 CC KW Antibiotic; Bacteriocin; Hydrolase; Endonuclease; Zinc; Metal-binding;
 KW Complete proteome.
 FT FT INIT_MET 0 0 ZINC (BY SIMILARITY).
 FT FT METAL 655 655 ZINC (BY SIMILARITY).
 FT FT METAL 680 680 ZINC (BY SIMILARITY).
 FT FT METAL 684 684 ZINC (BY SIMILARITY).
 FT FT CONFLICT 604 604 R -> RR (IN REF. 1).
 SQ SEQUENCE 688 AA; 7372 MW; 1EB45076A75352F1 CRC64;

Query Match 2.3%; Score 7; DB 1; Length 688;
 Best Local Similarity 100.0%; Pred. No. 84;
 Matches 28 LIGAVNL 34
 Qy 28 LIGAVNL 34
 Db 366 LIGAVNL 372
 RESULT 31

DR SMART; SMO0460; TGC; 1.
 DR PROSITE; PS00517; TRANSGLUTAMINASES; 1.
 KW Transferase; Acyltransferase; Calcium-binding.
 INIT MFT 0
 FT MOD RES 0
 FT ACT SITE 0
 FT ACT SITE 1
 FT ACT SITE 286 286 BY SIMILARITY.
 FT ACT SITE 344 344 BY SIMILARITY.
 FT ACT SITE 367 367 BY SIMILARITY.
 FT METAL 407 407 CALCIMUM (BY SIMILARITY).
 FT METAL 409 409 CALCIUM (BY SIMILARITY).
 FT METAL 455 455 CALCIUM (BY SIMILARITY).
 FT METAL 460 460 CALCIUM (BY SIMILARITY).
 SEQUENCE 697 AA; FB6916C9B4A42643 CRC64;
 SQ SEQUENCE 697 AA; 78608 MW; D341DB9C1988C2C8 CRC64;

Query Match 2.3%; Score 7; DB 1; Length 697;
 Best Local Similarity 100.0%; Pred. No. 85;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 RRLLCAR 14
 Db 514 RRLLCAR 520

RESULT 34
 YJYI_ECOLI STANDARD; PRT; 721 AA.
 AC P39376; (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 01-FEB-1995 (Rel. 41, Last annotation update)
 DT 28-FEB-2003 (Rel. 41, Last hypothetical protein YJYI)
 DE Hypothetical protein YJYI.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OC NCBITaxon:562;
 RN STRAIN="K12 / MG1655";
 RX MEDLINE=93334362; PubMed=7610040;
 RA Burland V.D., Plumkett G. III, Sofia H.J., Daniels D.L.,
 RA Blattner F.R.,
 RT "Analysis of the Escherichia coli genome VI: DNA sequence of the
 RT region from 92.8 through 100 minutes.";
 RL Nucleic Acids Res 23:2107-2119(1995).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
 CC (Potential).
 CC -!- SIMILARITY: BELONGS TO THE CSTA FAMILY.

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CC DR EMBL; AE000506; AAC77310.1; -.
 CC DR PIR; SS6580; SS6580.
 CC DR Ecogene; EG12516; YJYI.
 CC DR InterPro; IPR003706; CstA.
 CC DR Pfam; PF02554; CstA; 1.
 CC KW Hypothetical protein; Transmembrane; Inner membrane;
 CC Complete proteome.
 FT TRANSMEM 11 31 POTENTIAL.
 FT TRANSMEM 36 56 POTENTIAL.
 FT TRANSMEM 94 114 POTENTIAL.
 FT TRANSMEM 125 145 POTENTIAL.
 FT TRANSMEM 169 189 POTENTIAL.
 FT TRANSMEM 197 217 POTENTIAL.
 FT TRANSMEM 228 248 POTENTIAL.
 FT TRANSMEM 263 283 POTENTIAL.

RESULT 35
 SC18_YEAST STANDARD; PRT; 758 AA.
 ID SC18_YEAST
 AC P18759; (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 30, Last sequence update)
 DT 01-OCT-1994 (Rel. 42, Last annotation update)
 DE Vesicular-fusion protein SEC18.
 GN SEC18 OR YBR080C OR YBR0736.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetes;
 OC Saccharomycetales; Saccharomyces; Saccharomyces.
 [1] NCBI_TAXID=4932;
 RN SEQUENCE FROM N.A.
 RP MEDLINE=98039841; PubMed=1054509;
 RX RA Eakle K.A., Bernstein M., Emr S.D.;
 RT "Characterization of a component of the yeast secretion machinery:
 RT identification of the SEC18 gene product.";
 RL MoL Cell. Biol. 8:4098-4109(1998).
 RN SEQUENCE FROM N.A.
 RC STRAIN=S288C;
 RX RA van der Aart Q.J.M., Barttne C., Daignon F., Aigle M., Crouzet M.,
 RA Steenma H.Y.;
 RA "Sequence analysis of a 31 kb DNA fragment from the right arm of
 RT Saccharomyces cerevisiae chromosome II.";
 RL Yeast 10:959-964 (1994).
 [2] RN SEQUENCE OF 566-758 FROM N.A.
 RP SEQUENCE OF 566-758 FROM N.A.
 RC STRAIN=W303;
 RA Vornlocher H.-P., Hanachi P., Hershey J.W.B.;
 RA Vornlocher H.-P., Hanachi P., Hershey J.W.B.;
 RL SUBUNIT: Binds to SEC17.
 CC -!- FUNCTION: REQUIRED FOR VESICLE-MEDIATED TRANSPORT. CATALYZES THE
 CC FUSION OF TRANSPORT VESICLES WITHIN THE GOLGI CISTERNAE. IS ALSO
 CC REQUIRED FOR TRANSPORT FROM THE ENDOPLASMIC RETICULUM TO THE GOLGI
 CC STACK. SEEM TO FUNCTION AS A FUSION PROTEIN REQUIRED FOR THE GOLGI
 CC DELIVERY OF CARGO PROTEINS TO ALL COMPARTMENTS OF THE GOLGI STACK
 CC INDEPENDENT OF VESICLE ORIGIN.
 CC -!- SUBUNIT: Binds to SEC17.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: BELONGS TO THE AAA FAMILY OF ATPASES.

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 CC DR EMBL; M20662; AA335030; 1.
 CC DR EMBL; M20662; AA335030; 1.

DR EMBL; X76294; CAA53939.1; -.
 DR EMBL; S235939; CAA8505.1; -.
 DR EMBL; AF004912; AAB82417.1; -.
 PIR; S45477; S45477.
 DR PDB; 22-DIC18.
 SGD; S0000284; SEC18.
 DR GO; GO:0019897; :extrinsic_to_plasma_membrane; IDA.
 DR GO; GO:0004002; F:adenosine_inheritance; IDA.
 DR GO; GO:0000011; P:vacuole_inheritance; IDA.
 DR InterPro; IPR00593; AAA_ATPase.
 DR InterPro; IPR003959; AAA_ATPase_centr.
 DR InterPro; IPR003960; AAA_sub.
 DR InterPro; IPR003338; ATPaseATP_N.
 DR InterPro; IPR004201; Cdc48_2.
 DR Pfam; PF00004; AAA; 2.
 DR Pfam; PF02333; cdc48_2; 1.
 DR Pfam; PF02359; cdc48_N; 1.
 DR SMART; SM00382; AAA; 2.
 PROSITE; PS00674; AAA; 1.
 DR ATP-binding; Repeat; 3D-structure.
 KW ATP-binding; Repeat; Endoplasmic reticulum; Golgi stack;
 FT NP-BIND 281 288 ATP (POTENTIAL).
 FT NP-BIND 564 571 ATP (POTENTIAL).
 FT CONFLICT 381 381 MISSING (IN REF. 1).
 SQ SEQUENCE 758 AA; 84056 MW; AD6C677EA3674B3C CRC64;
 Query Match 2.3%; Score 7; DB 1; Length 758;
 Best Local Similarity 100.0%; Pred. No. 91;
 Matches 7; Conservative 0; Mismatches 0; Gaps 0;
 Qy 32 VNLIKSEN 38
 Db 214 VNLIKSEN 220
 RESULT 36
 CC16_YEAST ID CC16 YEAST STANDARD; PRT; 840 AA.
 AC P09798.
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DE Cell division control protein 16.
 GN CDC16 OR YKL022C.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;
 RN SEQUENCE FROM N.A.
 RP STRAIN=R.B.Wickner 1385;
 RC MEDLINE=88040465 PubMed=2823230;
 RX Ichio T.; Wickner R.B.;
 RT "Metal binding, nucleic acid-binding finger sequences in the CDC16 gene of *Saccharomyces cerevisiae*";
 RT *Nucleic Acids Res.* 15:8439-8450(1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Rieger M.;
 RL Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP REPEATS.
 RX MEDLINE=90124639; PubMed=204612;
 RA Sikorski R.S., Boguski M.S., Goebel M., Hietter P.A.;
 RT "A repeating amino acid motif in Cdc23 defines a family of proteins and a new relationship among genes required for mitosis and RNA synthesis";
 RT *Cell* 60:307-317(1990).
 RN [4]
 RP SUBUNITS.
 RX MEDLINE=95009933; PubMed=7925276;
 RA Lamb J.R., Michaud W.A., Sikorski R.S., Hietter P.A.;
 RT "Cdc15p, Cdc23p and Cdc27p form a complex essential for mitosis.";
 RN [2]
 RL EMBO J. 13:4321-4328 (1994).
 CC -!- FUNCTION: EXACT FUNCTION NOT KNOWN, REQUIRED FOR CHROMOSOME SEGREGATION. MUTATIONS IN CDC16 CAUSE CELLS TO ARREST UNIFORMLY AT G2/M AFTER DNA REPLICATION BUT PRIOR TO MITOTIC SPindle.
 CC -!- SUBUNIT: CDC16, CDC23 AND CDC27 FORMS A MACROMOLECULAR COMPLEX.
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- SIMILARITY: Contains 10 TPR repeats.
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 CC EMBL; X06165; CAA29321.1; -.
 DR EMBL; Z28022; CAA81857.1; -.
 DR PIR; A27832; A27832.
 DR SGD; S0001505; CDC16.
 DR InterPro; IPR001440; TPR.
 DR PFAM; PF00515; TPR_7.
 DR SMART; SM00028; TPR_6.
 KW Cell division; Cell cycle; Mitosis; Repeat; TPR repeat; TPR 1.
 KW Nucleolar Protein.
 FT REPEAT 263 295 TPR 1.
 FT REPEAT 296 329 TPR 2.
 FT REPEAT 359 392 TPR 3.
 FT REPEAT 497 530 TPR 4.
 FT REPEAT 531 564 TPR 5.
 FT REPEAT 565 598 TPR 6.
 FT REPEAT 599 632 TPR 7.
 FT REPEAT 633 666 TPR 8.
 FT REPEAT 674 707 TPR 9.
 SQ SEQUENCE 840 AA; 94991 MW; A036B34441083488 CRC64;
 Query Match 2.3%; Score 7; DB 1; Length 840;
 Best Local Similarity 100.0%; Pred. No. 99;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 33 NLKSSNR 39
 Db 30 NLKSSNR 36
 RESULT 37
 RPS2_ARATH ID RPS2_ARATH STANDARD; PRT; 909 AA.
 AC Q42484; 082096; QBL3R0; QBL4X9; QBL4Y0; QBL5B7; QBL5B3;
 AC QBL2Z8; QBLKZ9; QBL100; QASPS5;
 DT 15-SEP-2003 (Rel. 42, Created)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Disease resistance protein RPS2 (Resistance to *Pseudomonas syringae* protein 2).
 DE RPS2 OR AT4G26090 OR F20B18_200.
 GN Arabidopsis thaliana (Mouse-ear cress).
 OS Eukaryota; Viridiplantae; Strptophyta; Embryophyta; Tracheophyta;
 OC Specmatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=N.Cv. Columbia;
 RX MEDLINE=94377978; PubMed=8091210;
 RA Bent A.P., Kunkel B.N., Dahlbeck D., Brown K.L., Schmidt R., Giraudat J., Leung J., Staskiewicz B.J.;
 RA "RPS2 of Arabidopsis thaliana: a leucine-rich repeat class of plant disease resistance genes";
 RT Science 265:1856-1860(1994).
 RN [2]

- RP SEQUENCE FROM N.A., AND VARIANTS.
 RC STRAIN=cv. Columbia; PubMed=7923358;
 RX MEDLINE=95007758; PubMed=7923358;
- RA Mindrinos M., Katajiri F., Yu G.-L., Ausubel F.M.;
 RT "The *A. thaliana* disease resistance gene RPS2 encodes a protein
 containing a nucleotide-binding site and leucine-rich repeats.";
 RT Cell 78:1089-1098(1994).
 RN [3]
- RP SEQUENCE FROM N.A., AND VARIANTS.
 RC STRAIN=cv. Po-1;
 RX MEDLINE=12231631; PubMed=11333251;
 RA Banerjee D., Zhang X., Bent A.F.;
 RT "The leucine-rich repeat domain can determine effective interaction
 between RPS2 and other host factors in Arabidopsis RPS2-mediated
 disease resistance.";
 RT Genetics 158:439-450(2001).
 RN [4]
- RP SEQUENCE FROM N.A., AND VARIANTS.
 RC STRAIN=cv. Ab-7, cv. Ang-0, cv. Bg-4, cv. Bla-2, cv. Bur-0, cv. C2-1,
 CV. Co-1, cv. Ct-1, cv. Cv-0, cv. D2-9, cv. Fm-17, cv. G2-1,
 CV. Gott-20, cv. Gr-6, cv. Hs-12, cv. Kas-1, cv. KNO2, cv. Mt-0,
 CV. Tamm-17, cv. Tsu-0, cv. Po-1, cv. Pog-0, cv. Pu-8, cv. RLD,
 RC CV. Yo-0, cv. Wu-0, and cv. Zu-0;
 RX MEDLINE=22305406; PubMed=1261810;
 RA Mauricio R., Stahl E.A., Korves T., Tian D., Kreitman M.,
 RT "Natural selection for polymorphism in the disease resistance gene
 rps2 of *Arabidopsis thaliana*.";
 RL Genetics 163:735-746(2003).
 RN [5]
- RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=20083488; PubMed=10617198;
- RA Mayer K.F.X., Schueler C., Wambutt R., Murphy G., Volckaert G.,
 RA Pohl T., Duisterhoeft A., Stiedem W., Entian K.-D., Terry N.,
 RA Harris B., Ansorge W., Brandt P., Grivell L.A., Rieger M.,
 RA Weichselgartner M., de Simone V., Obermaier B., Mache R., Mueller M.,
 RA Kreis M., Delsing M., Puigdomenech P., Watson M., Schmidtheini T.,
 RA Reichert B., Portetelle D., Perez-Alonso M., Boutte M., Bancroft I.,
 RA Vos P., Hoheisel J., Zimmermann W., Wedler M., Ridley P.,
 RA Langham S.-A., McCullagh B., Bilham J., Robben J.,
 RA Van der Schueren J., Grimonprez B., Chuang Y.-J., Vandenburghe F.,
 RA Braeken M., Weijts J., Voet M., Bastiaens I., Aert R., Defoor E.,
 RA Weitzengenger T., Bothe G., Ramsperger U., Hilbert H., Braun M.,
 RA Holzer E., Brandt A., Peters S., van Staveren M., Dirkske W.,
 RA Moormann P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
 RA Bernerse S., Tempel S., Feldpausch M., Lambirth S., van den Daele H.,
 RA De Keyser A., Buysshaert C., Gielen J., Villarroel R., De Clercq R.,
 RA Montagut M., Rogers J., Hall J., Cronin A., Quail M., Bray-Allen S.,
 RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McLay K., Mayes R.,
 RA Petett A., Rajandream M.A., Bork P., Schatz M., Rechmann S.,
 RA Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fartmann B., Grandjean K., Dauner D., Herzel A.,
 RA Massenet O., Argirou F., Clabauld G., Piravandi E.,
 RA Schnabl S., Hiller R., Schmidt W., Lecharny A., Felber R.,
 RA Chefford R., Cooke R., Berger C., Casicuberta E.,
 RA Gibbons T., Weber N., Vandenberg M., Baiges M., Terol J., Torres A.,
 RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
 RA Heinen L., Schwarz S., Schoeller P., Heber S., Francis P., Bielke C.,
 RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
 RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
 RA Parneil L., Dediha N., Schutz K., Huang E., Spiegel L.,
 RA Sekhon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,
 RA Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J.,
 RA Latrille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
 RA Minx P., Bentley D., Fulton L., Miller N., Greco T., Kemp K.,
 RA Kramer J., Fulton L., Mardis R., Dante M., Pepin K., Hillier L.,
 RA Nelson J., Spieh J., Ryan E., Andrews S., Geisel C., Layman D.,
 RA Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joshi C.,
 RA Antoniou B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
 RA Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R.
- RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S.,
 RA Grant S., Shohdy N., Hameed A., Lodi N., Johnson A.,
 RA Chen E., Marra M., Martensen R., McCombie W.R.;
 RT "Sequence and analysis of Chromosome 4 of the plant *Arabidopsis*
thaliana.";
 RT Cell 40:769-777(1999).
 RN [6]
- RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=9833518; PubMed=9670562;
 RA Speilman E., Bouchez D., Holub E.B., Beynon J.L.;
 RT "Disease resistance gene homologs correlate with disease resistance
 loci of *Arabidopsis thaliana*.";
 RT Plant J. 14:467-474 (1995).
 RN [7]
- RP SEQUENCE OF 184-352 FROM N.A.
 RC STRAIN=cv. Nd-1;
 RX MEDLINE=9714059; PubMed=8986840;
 RA Subcellular location, and mutagenesis of ILE-353.
 RX MEDLINE=9714059; PubMed=8986840;
 RA Leister R.T., Ausubel F.M., Katajiri F.;
 RT "Molecular recognition of pathogen attack occurs inside of plant cells
 in plant disease resistance specified by the *Arabidopsis* genes RPS2
 and RPM1.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:15497-15502 (1996).
 RN [8]
- RP IDENTIFICATION IN A COMPLEX CONTAINING AVRPT2 AND AVR-B.
 RX MEDLINE=0307433; PubMed=10849351;
 RA Leister R.T., Katajiri F.;
 RT "A resistance gene product of the nucleotide binding site -- leucine
 rich repeats class can form a complex with bacterial avirulence
 proteins in vivo.";
 RT Plant J. 22:345-354 (2000).
 RN [9]
- RP MUTAGENESIS OF 38-LEU-THR-40; LYS-188; THR-189; THR-190 AND
 RA Pohl T., Duesterhoeft A., Stiedem W., Entian K.-D., Terry N.,
 RA Harris B., Ansorge W., Brandt P., Grivell L.A., Rieger M.,
 RA Weichselgartner M., de Simone V., Obermaier B., Mache R., Mueller M.,
 RA Kreis M., Delsing M., Puigdomenech P., Watson M., Schmidtheini T.,
 RA Reichert B., Portetelle D., Perez-Alonso M., Boutte M., Bancroft I.,
 RA Vos P., Hoheisel J., Zimmermann W., Wedler M., Ridley P.,
 RA Langham S.-A., McCullagh B., Bilham J., Robben J.,
 RA Van der Schueren J., Grimonprez B., Chuang Y.-J., Vandenburghe F.,
 RA Braeken M., Weijts J., Voet M., Bastiaens I., Aert R., Defoor E.,
 RA Weitzengenger T., Bothe G., Ramsperger U., Hilbert H., Braun M.,
 RA Holzer E., Brandt A., Peters S., van Staveren M., Dirkske W.,
 RA Moormann P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
 RA Bernerse S., Tempel S., Feldpausch M., Lambirth S., van den Daele H.,
 RA De Keyser A., Buysshaert C., Gielen J., Villarroel R., De Clercq R.,
 RA Montagut M., Rogers J., Hall J., Cronin A., Quail M., Bray-Allen S.,
 RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McLay K., Mayes R.,
 RA Petett A., Rajandream M.A., Bork P., Schatz M., Rechmann S.,
 RA Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fartmann B., Grandjean K., Dauner D., Herzel A.,
 RA Massenet O., Argirou F., Clabauld G., Muendlein A., Felber R.,
 RA Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,
 RA Chefford R., Cooke R., Berger C., Casicuberta E.,
 RA Gibbons T., Weber N., Vandenberg M., Baiges M., Terol J., Torres A.,
 RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
 RA Heinen L., Schwarz S., Schoeller P., Heber S., Francis P., Bielke C.,
 RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
 RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
 RA Parneil L., Dediha N., Schutz K., Huang E., Spiegel L.,
 RA Sekhon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,
 RA Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J.,
 RA Latrille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
 RA Minx P., Bentley D., Fulton L., Miller N., Greco T., Kemp K.,
 RA Kramer J., Fulton L., Mardis R., Dante M., Pepin K., Hillier L.,
 RA Nelson J., Spieh J., Ryan E., Andrews S., Geisel C., Layman D.,
 RA Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joshi C.,
 RA Antoniou B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
 RA Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R.
- RA "Arabidopsis RIN4 is a target of the type III virulence effector
 AvrP2 and modulates RPS2-mediated resistance.";
 RT Cell 112:379-389(2003).
 RL [12]
- I- FUNCTION: Disease resistance (R) protein that specifically
 recognizes the AvrP2 type III effector avirulence protein from
 Pseudomonas syringae. Resistance proteins guard the plant against
 pathogens that contain an appropriate avirulence protein via an
 indirect interaction with this avirulence protein. That triggers a
 defense system including the hypersensitive response, which

restricts the pathogen growth. Acts via its interaction with RIN4, CC and probably triggers the plant resistance when RIN4 is degraded by AvrRp2.

-|- SUBUNIT: Interacts indirectly with RIN4. Found in a complex with AvrRp2 and AvrB.

CC -|- SUBCELLULAR LOCATION: Cytoplasmic; membrane-associated.

-|- DOMAIN: The LRR repeats probably act as specificity determinant of pathogen recognition (By similarity).

-|- DOMAIN: The leucine-zipper domain is essential for the resistance to AvrRp2; the cultivars that do not display resistance showing specific variations in this region.

-|- POLYMORPHISM: The polymorphism between the different cultivars Po-1, KNO2, BG-4 and Zu-0, RPS2 does not confer resistance to AvrRp2.

-|- SIMILARITY: Belongs to the disease resistance NB-LRR family.

-|- SIMILARITY: Contains 6 leucine-rich (LRR) repeats.

-|- SIMILARITY: Contains 1 NB-ARC domain.

-|- DATABASE: NAME=NIB-LRSS;

-|- FUNCTIONAL AND COMPARATIVE GENOMICS OF DISEASE RESISTANCE GENE HOMOLOGS; [www="http://www.ncbi.nlm.nih.gov"](http://www.ncbi.nlm.nih.gov).

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Query Match Score 7; DB 1; Length 909;
Best Local Similarity 100.0%; Pred No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 256 LalitLG 262
Db 350 LalitLG 356

RESULT 38
SCA4_RICFE ID SCA4_RICFE STANDARD; PRT; 981 AA.
AC Q9AJ37;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Antigenic heat-stable 120 kDa protein (PS120) (1120 kDa antigen)
DE (Protein PS 120) (Fragment)
GN SCA4 OR D.
OS Rickettsia felis (Rickettsia azadii).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_TaxID42862,
RN [1]
RP SEQUENCE FROM N.A.

RA Sekeyova Z.; Roux V.; Raoult D.;
RT "Phylogenetic analysis of Rickettsia spp. by comparing the sequence of gene D coding for an intracytoplasmic protein.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
-|- SUBCELLULAR LOCATION: Cytoplasmic (Probable).

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CC DR EMBL; AF196973; AAK31304.1; -.
KW Antigen.
FT 1 1

CC FT NON_TER SEQENCE ID K6P1_CANAL STANDARD; PRT; 981 AA; 107514 MW; 7E18F421E2C262E1 CRC64;
CC Query Match Score 7; DB 1; Length 981;
CC Best Local Similarity 100.0%; Pred. No. 1.1e+02;
CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 57 DSQTDDP 63
Db 57 DSQTSDDP 63

RESULT 39
K6P1_CANAL ID K6P1_CANAL STANDARD; PRT; 987 AA.
AC 094261;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE 6-phosphofructokinase alpha subunit (EC 2.7.1.11) (Phosphofructokinase 1) (Phosphohexokinase) (PFK-1-K alpha subunit) (CaPFK1).
DE 1) (Phosphofructokinase 1) (Phosphohexokinase) (PFK-1-K alpha subunit) (CaPFK1).
GN PFK1.
OS Candida albicans (Yeast).
OC Bacteria; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomyctales; Candidida.

CC SEQUENCE FROM N.A., AND CHARACTERIZATION.
NCBI_TAXID=5476;

RN [1]
RP MEDLINE=99191002; PubMed=10091602;
RX Lorberg A., Karchrath L., Ernst J.F., Heinisch J.J.;
RA "Genetic and biochemical characterization of phosphofructokinase from the opportunistic pathogenic yeast Candida albicans." Eur. J. Biochem. 260:217-226(1999).

-|- CATALYTIC ACTIVITY: ATP + D-fructose 6-phosphate = ADP + D-fructose 1,6-bisphosphate.

-|- ENZYME REGULATION: Allosterically inhibited by ATP and activated by AMP and fructose 2,6-bisphosphate.

-|- PATHWAY: Key control step of glycolysis.

-|- SUBUNIT: Heterooctamer of 4 alpha and 4 beta chains (By similarity).

-|- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

-|- SIMILARITY: Belongs to the phosphofructokinase family. Two domains CC subfamily.

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CC DR EMBL; AJ007638; CAB38868.1; -.
DR HSSP; P00512; 3PFK.
DR InterPro; IPR00023; PfFrckinase.
DR Pfam; PF00365; PEK_2.
DR PRINTS; PR00476; PHFRCKINASE.
DR PRODom; PD000707; PfFrckinase_2.
DR PROSITE; PS00033; PHOSPOFRUCTOKINASE_1.
KW Kinase; Transferase; Glycolysis; Repeat; Allosteric enzyme.
SEQUENCE 987 AA; 108577 MW;

CC DR Query Match Score 7; DB 1; Length 987;
CC Best Local Similarity 100.0%; Pred. No. 1.1e+02;
CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 233 QEMEVVD 239
Db 91 QEMEVVD 97

RESULT 40

SCA4_RICSI STANDARD; PRT; 991 AA.

ID SCA4_RICSI
AC Q9A377;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Antigenic heat-stable 120 kDa protein (PS120) (120 kDa antigen)
(Protein PS 120) (Fragment).
GN SCA4 OR D.
OS Rickettsia sibirica.
Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Rickettsiae; Rickettsia.
NCBI_TaxID=35733;
RN [1]
RP SEQUENCE FROM N.A.
RA Sekeyova Z., Roux V., Raoult D.;
RT "Phylogenetic analysis of Rickettsia spp. by comparing sequence of the
'gene D' coding for an intracytoplasmic protein';
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to licensee@isb-sib.ch).
CC
DR EMBL; AF155057; AAK30688.1; -.
KW Antigen.
PT NON-TER 1 991
FT NON-TER 1 991
SEQUENCE 991 AA; 108564 MW; 3F499934933D15C CRC64;
Query Match 2.3%; Score 7; DB 1; Length 991;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 57 DSQTSVP 63
Db 67 DSQTSVP 73

RESULT 42
SCA4_RICMN STANDARD; PRT; 1011 AA.

ID SCA4_RICMN
AC Q9A380;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Antigenic heat-stable 120 kDa protein (PS120) (120 kDa antigen)
(Protein PS 120) (Fragment).
GN SCA4 OR D.
OS Rickettsia mongolotimonae.
Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Rickettsiae; Rickettsia.
NCBI_TaxID=45261;
RN [1]
RP SEQUENCE FROM N.A.
RA Sekeyova Z./, Roux V., Raoult D.;
RT "Phylogenetic analysis of Rickettsia spp. by comparing sequence of the
'gene D' coding for an intracytoplasmic protein.';
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
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or send an email to licensee@isb-sib.ch).
CC
DR EMBL; AF151725; AAK30683.1; -.
KW Antigen.
PT NON-TER 1 1011
FT NON-TER 1 1011
SEQUENCE 1011 AA; 110607 MW; 0169A06981BD5D08 CRC64;
Query Match 2.3%; Score 7; DB 1; Length 1011;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 57 DSQTSVP 63
Db 67 DSQTSVP 73

RESULT 43
SCA4_RICSL STANDARD; PRT; 1012 AA.

ID SCA4_RICSL
AC Q9A380;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Antigenic heat-stable 120 kDa protein (PS120) (120 kDa antigen)
(Protein PS 120) (Fragment).
GN SCA4 OR D.
OS Rickettsia africae.
Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Rickettsiae; Rickettsia.
NCBI_TaxID=35733;
RN [1]
RP SEQUENCE FROM N.A.
RA Sekeyova Z., Roux V., Raoult D.;
RT "Phylogenetic analysis of Rickettsia spp. by comparing sequence of the
'gene D' coding for an intracytoplasmic protein.';
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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or send an email to licensee@isb-sib.ch).

OC Rickettsiaceae; Rickettsiae; Rickettsia.
 OC NCBI_TaxID=781;
 RN [1] SEQUENCE FROM N.A.
 RP STRAIN-Malib7;
 RC MEDLINE=94156485; PubMed=8112862;
 RX Schuenke K.W., Walker D.H.,
 RA "Cloning, sequencing, and expression of the gene coding for an
 RT antigenic 20-kilodalton protein of *Rickettsia conorii*.";
 RT Infect. Immun. 62:904-909 (1994).
 RL [2]
 RN RP
 SEQUENCE FROM N.A.
 STRAIN-Malib7;
 RX MEDLINE=21442074; PubMed=11557893;
 RA Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,
 RA Samson D., Roux V., Cossart P., Weissbach J., Claverie J.-M.,
 RA Raoult D.;
 RT "Mechanisms of evolution in *Rickettsia conorii* and R. prowazekii.";
 RL Science 293:2093-2098(2001).
 CC [-] SUBCELLULAR LOCATION: Cytoplasmic (Probable).

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CC SEQUENCE FROM N.A.
 DR EMBL; U01133; AA018636; 1; -;
 DR EMBL; AE008626; AAL0205; 1; ALT_INIT.
 KW Antigen; Complete protein; MW: 881042542B7B982 CRC64;
 SQ SEQUENCE 1022 AA; 111802 MW;

Query Match Score 7; DB 1; Length 1022;
 Best Local Similarity 2.3%; Pred. No. 1.2e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 57 DSQTSDP 63
 Db 74 DSQTSDP 80

RESULT 47
 ITA3 MOUSE STANDARD: PRT; 1053 AA.
 ID ITA3 MOUSE
 AC Q08441; Q08442;
 DT 15-JUL-1998 (Rel. 36; Created)
 DT 15-JUL-1998 (Rel. 36; Last sequence update)
 DT 28-FEB-2003 (Rel. 41; Last annotation update)
 DB Integrin alpha-3 precursor (Galactoprotein B3) chain (CD49c).
 DE ITG43.
 OS Mus musculus. (Mouse)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090.
 RN [1] SEQUENCE FROM N.A.
 RP STRAIN=BALB/C;
 RX MEDLINE=95279462; PubMed=7759572;
 RA Takeuchi K., Hirano K., Tuji T., Obama T., Irimura T.;
 RT "cDNA cloning of mouse VLA-3 alpha subunit.";
 RL J. Cell. Biochem. 57:371-377 (1995).
 RN [2] SEQUENCE OF 913-1053 FROM N.A., AND ALTERNATIVE SPlicing.
 RP MEDLINE=92052235; PubMed=194648;
 RX Tamura R.N., Cooper H.M., Collo G., Quaranta V.;
 RT "Cell type-specific integrin variants with alternative alpha chain
 cytoplasmic domains";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:10183-10187 (1991).
 CC [-] FUNCTION: INTEGRIN ALPHA-3/BETA-1 IS A RECEPTOR FOR FIBRONECTIN,
 LAMININ, COLLAGEN, EPILIGRIN AND THROMBOSPONDIN.

CC [-] SUBUNIT: HETERO-DIMER OF AN ALPHA AND A BETA SUBUNIT. THE ALPHA SUBUNIT IS COMPOSED OF AN HEAVY AND A LIGHT CHAIN LINKED BY A DISULFIDE BOND. ALPHA-3 ASSOCIATES WITH BETA-1.
 CC [-] SUBCELLULAR LOCATION: Type I membrane protein.
 CC [-] ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=2;
 CC Name=Alpha-3A;
 CC IsoId=Q62470-1; Sequence=Displayed;
 CC Name=Alpha-3B;
 CC IsoId=Q62470-2; Sequence=VSP 002722;
 CC [-] SIMILARITY: BELONGS TO THE INTEGRIN ALPHA CHAIN FAMILY.

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CC SEQUENCE FROM N.A.
 DR EMBL; D13867; BAA03980; 1; -;
 DR EMBL; S66792; AAB20356; 2; -;
 DR EMBL; S66294; AAB20357; 2; -;
 DR PRINTS; PR00357; integrin_A; 1.
 DR SMART; SM00191; Int_alpha; 5;
 DR PROSITE; PS00242; INTEGRIN_ALPHA; 1.
 DR InterPro; IPR000413; Integrin_alpha.
 DR Pfam; PF01839; FG_GAP; 3;
 DR Pfam; PF00357; integrin_A; 1.
 DR PRINTS; PR01185; INTEGRINA.
 DR SMART; SM00191; Int_alpha; 5;
 DR PROSITE; PS00242; INTEGRIN_ALPHA; 1.
 KW Integrin; Cell adhesion; Glycoprotein; Transmembrane; Signal; Repeat; KW Alternative splicing
 FT SIGNAL 1 32 BY SIMILARITY.
 FT CHAIN 33 1053 INTERIN ALPHA-3.
 FT CHAIN 33 874 INTERIN ALPHA-3 HEAVY CHAIN (POTENTIAL).
 FT CHAIN 878 1053 INTERIN ALPHA-3 LIGHT CHAIN (POTENTIAL).
 FT DOMAIN 33 993 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 994 1021 POTENTIAL.
 FT DOMAIN 1022 1053 CYTOPLASMIC (POTENTIAL).
 FT REPEAT 49 94 7 X APPROXIMATE REPEATS.
 FT REPEAT 120 165 I.
 FT REPEAT 195 227 III.
 FT REPEAT 246 280 IV.
 FT REPEAT 305 346 V.
 FT REPEAT 367 403 VI.
 FT REPEAT 427 462 VII.
 FT DISULFID 94 103 BY SIMILARITY.
 FT DISULFID 140 162 BY SIMILARITY.
 FT DISULFID 185 197 BY SIMILARITY.
 FT DISULFID 486 491 BY SIMILARITY.
 FT DISULFID 497 551 BY SIMILARITY.
 FT DISULFID 616 622 BY SIMILARITY.
 FT DISULFID 695 704 BY SIMILARITY.
 FT DISULFID 848 906 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 913 918 BY SIMILARITY.
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 86 86 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 501 501 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 512 512 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 574 574 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 606 606 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 657 657 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 699 699 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 843 843 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 859 859 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 925 925 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 928 928 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 937 937 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 971 971 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPIC 1023 1053 RARTAVALYEAKRQKEMKSQPSSETRLRLLDDY -> PTRRYR IMPKTHAVR TREEDDYPPGSPSTLPPTKKHW (in isoform

PT Alpha-3B).
 FT /FTId=ISP 002722.
 FT CONFLICT 975 975 W->C (IN REF. 2).
 FT CONFLICT 979 979 D->N (IN REF. 2).
 FT CONFLICT 1002 1002 G->S (IN REF. 2).
 FT CONFLICT 1019 1019 G->D (IN REF. 2).
 SQ SEQUENCE 1053 AA; 116745 MW; 645E8FBDBA86D6E5 CRC64;

Query Match Score 7; DB 1; Length 1053;
 Best Local Similarity 100.0%; Pred. No. 1.e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | |
|----------------|-------------------|
| Qy 4 RPPRLR 10 | Db 525 RPPRLR 531 |
|----------------|-------------------|

RESULT 48
 ITA3_CRISP ID ITA3 CRISP STANDARD; PRT; 1066 AA.
 AC P17852; DT 01-NOV-1990 (Rel. 16, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Integrin alpha-3 precursor (Galactoprotein B3) (GAPB3) (VLA-3 alpha chain) (CD49c).
 DE ITGA3.
 OS Crictidae sp. (Hamster).
 OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butelostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae.
 OM NCBI_TaxID=36483;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM ALPHA-3A), AND PARTIAL SEQUENCE.
 RC TISSUE(Fibroblast); MEDLINE=9016739; PubMed=1691184;
 RX RA Tsuji T., Yamamoto F.-I., Miura Y., Takio K., Pawar S.,
 RA Osawa T., Hakomori S.-I.; RT "Characterization through cDNA cloning of galactoprotein b3 (Gap b3), a cell surface membrane glycoprotein showing enhanced expression on oncogenic transformation. Identification of Gap b3 as a member of the integrin superfamily.";
 RT J. Biol. Chem. 265:7016-7021(1990).
 RN [2]
 RP ALTERNATIVE SPlicing.
 RX MEDLINE=92052235; PubMed=1946438;
 RA Tamura R.N., Cooper H.M., Collo G., Quaranta V.;
 RT "Cell type-specific integrin variants with alternative alpha chain cytoplasmic domains";
 RT Proc. Natl. Acad. Sci. U.S.A. 88:10183-10187(1991).
 CC -!- SUBUNIT, HETERO-DIMER OF AN ALPHA AND A BETA SUBUNIT. THE ALPHA SUBUNIT IS COMPOSED OF AN HEAVY AND A LIGHT CHAIN LINKED BY A DISULFIDE BOND. ALPHA-3 ASSOCIATES WITH BETA-A.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 Event=Alternative splicing; Named isoforms=2;
 CC Name=Alpha-3B;
 CC IsoId=P17852-1; Sequence=Displayed;
 CC Name=Alpha-3A;
 CC IsoId=P17852-2; Sequence=VSP 002720;
 CC Note=No experimental confirmation available;
 CC -!- PTM: ISOFORM ALPHA-3A BUT NOT ISOFORM ALPHA-B, IS PHOSPHORYLATED ON SERINE RESIDUES (BY SIMILARITY).
 CC -!- SIMILARITY: Contains 7 FG-GAP repeats.

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CC or send an email to license@isb-sib.ch).
 CC CC /FTId=ISP 002722;
 CC DR EMBL; J02281; AAA56794_1; -;
 CC DR HSSP; P11215; 1ABX.
 CC DR InterPro; IPR004041; Integrin_alpha.
 CC DR Pfam; PF01839; FG-GAP; 3.
 CC DR PRINTS; PRO1185; INTEGRINA.
 CC DR SMART; SM00191; Int alpha; 5.
 CC DR PROSITE; PS00242; INTEGRIN ALPHA; FALSE NEG KW Integrin; Cell adhesion; Receptor; Glycoprotein; Transmembrane; Signal; Phosphorylation; Repeat; Alternative splicing; Calcium.
 CC KW KW
 CC FT SIGNAL; 1 32
 CC FT CHAIN 33 1066
 CC FT CHAIN 33 872
 CC FT DOMAIN 33 1066
 CC FT DOMAIN 33 991
 CC FT REPEAT 49 1019
 CC FT REPEAT 49 1066
 CC FT REPEAT 49 94
 CC FT REPEAT 120 94
 CC FT REPEAT 195 227
 CC FT REPEAT 246 279
 CC FT REPEAT 304 345
 CC FT REPEAT 366 402
 CC FT REPEAT 426 461
 CC FT CA_BIND 315 323
 CC FT CA_BIND 378 386
 CC FT CA_BIND 439 447
 CC FT SITE 1017 1021
 CC FT DISULFID 94 103
 CC FT DISULFID 140 162
 CC FT DISULFID 185 197
 CC FT DISULFID 485 490
 CC FT DISULFID 496 550
 CC FT DISULFID 615 621
 CC FT DISULFID 694 702
 CC FT DISULFID 846 904
 CC FT CARBOHYD 86 86
 CC FT CARBOHYD 911 916
 CC FT CARBOHYD 986 986
 CC FT CARBOHYD 500 500
 CC FT CARBOHYD 511 511
 CC FT CARBOHYD 573 573
 CC FT CARBOHYD 605 605
 CC FT CARBOHYD 656 656
 CC FT CARBOHYD 697 697
 CC FT CARBOHYD 841 841
 CC FT CARBOHYD 923 923
 CC FT CARBOHYD 926 926
 CC FT CARBOHYD 935 935
 CC FT CARBOHYD 969 969
 CC FT VARSPIC 1021 1066
 CC FT RDRW -> RARTRAYEARQKARMKSQQSETERLDDY
 CC (in isoform Alpha-3A).
 CC /FTId=VSP 002720;
 CC /FTId=VSP 002720;
 CC SQ SEQUENCE 1066 AA; 118550 MW; ED089C2431E57684 CRC64;
 CC Query Match 2.3%; Score 7; DB 1; Length 1066;
 CC Best Local Similarity 100.0%; Pred. No. 1.e+02;
 CC Matches 7; Conservative 0; Mi.matches 0; Indels 0; Gaps 0;

RESULT 49
 ITA3_HUMAN
 ID ITA3_HUMAN
 AC P26006;
 DR 01-MAY-1992 (Rel. 22, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Integrin alpha-3 precursor (Galactoprotein B3) (GAPB3) (VLA-3 alpha

| | | |
|---|---|---|
| DE chain | (CD49c). | |
| GN ITGA3 | Homo sapiens (Human). | |
| DS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; | | |
| DC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | |
| NCBI TaxID=9606; | | |
| [1] FROM N.A. (ISOFORMS ALPHA-3A AND ALPHA-3B). | | |
| SEQUENCE MEDLINE#92011866; PubMed=1655803; | | |
| Takada Y., Murphy E., Pil P., Chen C., Ginsberg M.H., Hemler M.E.; "molecular cloning and expression of the cDNA for alpha 3 subunit of human alpha 3 beta 1 (VLA-3), an integrin receptor for fibronectin, laminin, and collagen."; | | |
| J. Cell Biol. 115:257-266 (1991). | | |
| [2] PARTIAL SEQUENCE FROM N.A. (ISOFORM ALPHA-3A). | | |
| TISSUE Tissue: fibroblast; MEDLINE#911311981; PubMed=1714443; | | |
| XX Tsuji T., Hakomori S.-I., Osawa T.; "Identification of human galactoprotein b3, an oncogenic transformation-induced membrane glycoprotein, as VLA-3 alpha subunit: the primary structure of human integrin alpha 3."; | | |
| [3] [4] PARTIAL SEQUENCE OF 33-46. | | |
| SEQUENCE MEDLINE#87204112; PubMed=3033641; | | |
| XX Takada Y., Strominger J.L., Hemler M.E.; "The very late antigen family of heterodimers is part of a superfamily of molecules involved in adhesion and embryogenesis."; | | |
| AA Proc. Natl. Acad. Sci. U.S.A. 84:3239-3243 (1987). | | |
| [4] ALTERNATIVE SPLICING, PHOSPHORYLATION, AND TISSUE SPECIFICITY. | | |
| RP MEDLINE#92265610; PubMed=9111516; | | |
| XX de Meijer A.A., Sterk L.M., Delwel G.O., Fles D.L., Daams H., Weening J.J., Sonnenberg A.; "The A and B variants of the alpha 3 integrin subunit: tissue distribution and functional characterization."; | | |
| AA Lab. Invest. 76:547-563 (1997). | | |
| -1- FUNCTION: INTEGRIN ALPHA-3/BETA-1 IS A RECEPTOR FOR FIBRONECTIN, LAMININ, COLLAGEN, EPILIGRIN AND THROMbospondin. | | |
| -1- SUBUNIT: Heterodimer of an alpha and a beta subunit. The alpha subunit is composed of an heavy and a light chain linked by a disulfide bond. Alpha-3 associates with beta-1. Interacts with HPSS. | | |
| CC -1- ALTERNATIVE PRODUCTS: | | |
| CC -1- ALTERNATIVE splicing; Named isoforms=2; | | |
| CC Name=Alpha-3B; | | |
| CC IsoID=p26006-1; Sequence=Displayed; | | |
| CC Name=Alpha-3A; | | |
| CC IsoID=p26006-2; Sequence=VSP 002721; | | |
| CC -1- TISSUE SPECIFICITY: ISOFORM ALPHA-3A IS WIDELY EXPRESSED. ISOFORM ALPHA-3B IS EXPRESSED IN BRAIN AND HEART. IN BRAIN, BOTH ISOFORMS ARE EXCLUSIVELY EXPRESSED ON VASCULAR SMOOTH MUSCLE CELLS, WHEREAS IN HEART ISOFORM ALPHA-3A IS STRONGLY EXPRESSED ON VASCULAR SMOOTH MUSCLE CELLS, ISOFORM ALPHA-3B IS DETECTED ONLY ON ENDOTHELIAL VENOUS CELLS. | | |
| CC -1- PTM: ISOFORM ALPHA-3A, BUT NOT ISOFORM ALPHA-3B, IS PHOSPHORYLATED ON SERINE RESIDUES. PHOSPHORYLATION INCREASES AFTER PHORBOL 12-MYRISTATE 13-ACTETATE STIMULATION. | | |
| CC -1- SIMILARITY: BELONGS TO THE INTEGRIN ALPHA CHAIN FAMILY. | | |
| CC -1- SIMILARITY: Contains 7 FG-GAP repeats. | | |
| CC -1- DATABASE: NAME=PROW; NOTE=CD Guide CD9c entry; WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd9c.htm". | | |
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| DR EMBL; M59911; AAA36120.1; -. | | |
| DR EMBL; D01038; BAA00845.1; -. | | |
| DR PIR; A40021; AA0021. | | |
| DR HSSP; P11215; IAX8. | | |
| DR Genew; HGNC:6139; ITGA3. | | |
| DR MIM; 602055; -. | | |
| DR GO; GO:00081305; C:integrin complex; TAS. | | |
| DR GO; GO:00081895; F:cell adhesion receptor activity; TAS. | | |
| DR GO; GO:0007160; P:cell-matrix adhesion; TAS. | | |
| DR Interpro; IPR00413; Integrin_alpha. | | |
| DR PRINS; PRO185; INTEGRINA. | | |
| DR SMART; SM0191; Int_alpha_5. | | |
| DR PROSITE; PS00242; INTEGRIN_ALPHA; 1. | | |
| KW Integrin; Cell adhesion; Receptor; Glycoprotein; Transmembrane; Signal; Phosphorylation; Repeat; Alternative splicing; Calcium. | | |
| KW SIGNAL 1 | | |
| FT DOMAIN 32 | | |
| FT CHAIN 33 | 1066 | INTEGRIN ALPHA-3 |
| FT CHAIN 33 | 872 | INTEGRIN ALPHA-3 HEAVY CHAIN (POTENTIAL). |
| FT CHAIN 33 | 1066 | INTEGRIN ALPHA-3 LIGHT CHAIN (POTENTIAL). |
| FT DOMAIN 33 | 991 | EXTRACELLULAR (POTENTIAL). |
| FT TRANSMEM 992 | 1014 | POTENTIAL. |
| FT DOMAIN 1015 | 1016 | CYTOSPLASMIC (POTENTIAL). |
| FT DOMAIN 1015 | 1021 | INTERACTION WITH HPSS. |
| FT REPEAT 49 | 94 | PG-GAP 1. |
| FT REPEAT 120 | 165 | PG-GAP 2. |
| FT REPEAT 195 | 227 | PG-GAP 3. |
| FT REPEAT 246 | 279 | PG-GAP 4. |
| FT REPEAT 304 | 345 | PG-GAP 5. |
| FT REPEAT 366 | 402 | PG-GAP 6. |
| FT REPEAT 426 | 461 | PG-GAP 7. |
| FT CA_BIND 315 | 323 | POTENTIAL. |
| FT CA_BIND 378 | 386 | POTENTIAL. |
| FT SITE 1017 | 1021 | GFPKR MOTIF. |
| FT DISULFID 94 | 103 | BY SIMILARITY. |
| FT DISULFID 140 | 162 | BY SIMILARITY. |
| FT DISULFID 185 | 197 | BY SIMILARITY. |
| FT DISULFID 485 | 490 | BY SIMILARITY. |
| FT DISULFID 496 | 550 | BY SIMILARITY. |
| FT DISULFID 615 | 621 | BY SIMILARITY. |
| FT DISULFID 694 | 702 | BY SIMILARITY. |
| FT DISULFID 846 | 904 | INTERCHAIN BY SIMILARITY. |
| FT DISULFID 911 | 916 | BY SIMILARITY. |
| FT CARBOHYD 86 | 86 | N-LINKED (GICNAC). (POTENTIAL). |
| FT CARBOHYD 107 | 107 | N-LINKED (GICNAC). (POTENTIAL). |
| FT CARBOHYD 265 | 265 | N-LINKED (GICNAC). (POTENTIAL). |
| FT CARBOHYD 500 | 500 | N-LINKED (GICNAC). (POTENTIAL). |
| FT CARBOHYD 511 | 511 | N-LINKED (GICNAC). (POTENTIAL). |
| FT CARBOHYD 573 | 573 | N-LINKED (GICNAC). (POTENTIAL). |
| FT CARBOHYD 605 | 605 | N-LINKED (GICNAC). (POTENTIAL). |
| FT CARBOHYD 656 | 656 | N-LINKED (GICNAC). (POTENTIAL). |
| FT CARBOHYD 697 | 697 | N-LINKED (GICNAC). (POTENTIAL). |
| FT CARBOHYD 841 | 841 | N-LINKED (GICNAC). (POTENTIAL). |
| FT CARBOHYD 857 | 857 | N-LINKED (GICNAC). (POTENTIAL). |
| FT CARBOHYD 926 | 926 | N-LINKED (GICNAC). (POTENTIAL). |
| FT CARBOHYD 935 | 935 | N-LINKED (GICNAC). (POTENTIAL). |
| FT VARSPLIC 1022 | 1066 | TRYQQIMPQTHAVRIRBEERYPPGSLPTPKHWTQTRDDY |
| FT | DOYY -> ARTALYEAKKROKEMKSQPSSETRLTDDY | (in isoform Alpha-3A). |
| FT | /FTid=SP 002721. | /FTid=SP 002721. |
| SQ SEQUENCE 1066 AA; | 118697 MW; | 18F008ECDFB8CE CRC64; |
| QY 4 RRRPRR 10 | | Query Match Score 7; DB 1; Length 1066; |
| Db 524 RRRPRR 530 | | Best Local Similarity 100.0%; Pred. No. 1.2e+02; Mismatches 0; Indels 0; Gaps |

RESULT 50
 YEGE_ECOLI STANDARD; PRT; 1105 AA.
 AC P38077; P76391;
 DT 01-OCT-1994 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DB HYPOTHETICAL_protein_yege.
 GN YEGE OR B2057.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 NCBI_TaxID:562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / MG1655;
 RX MEDLINE#=97426617; PubMed=9278503;
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 Mau B., Shao Y.;
 RT "The complete genome sequence of *Escherichia coli* K-12.";
 SCIENCE 277:1453-1474 (1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX STRAIN=K12;
 MEDLINE#=9751358; PubMed=9097040;
 RA Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T.,
 Isono K., Kasai H., Kimura S., Kitagawa M.,
 Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
 Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T.,
 Saito N., Sampei G., Seki Y., Sivasundaram S., Tagami H.,
 Takeda J., Takenoto K., Wada C., Yamamoto Y., Horikuchi T.;
 RT "A 460-kb DNA sequence of the *Escherichia coli* K-12 genome
 corresponding to the 40.1-50.0 min region on the linkage map.";
 RL DNA Res. 3:379-392 (1996).
 RN [3]
 RP SEQUENCE OF 965-1105 FROM N.A.
 RX MEDLINE#=85054800; PubMed=094528;
 RA Nakabepu Y., Miyata T., Kondo H., Iwanaga S., Sekiguchi M.;
 RT "Structure and expression of the alka gene of *Escherichia coli*
 involved in adaptive response to alkylating agents.";
 RL J. Biol. Chem. 259:13730-13736 (1984).
 RN [4]
 RP IDENTIFICATION
 RX MEDLINE#=95075659; PubMed=7984428;
 RA Borodovsky M., Rudd K.E., Koonin E.V.;
 RT "Intrinsic and extrinsic approaches for detecting genes in a
 bacterial genome."
 RL Nucleic Acids Res. 22:4767-4767 (1994).
 CC !- SIMILARITY: Contains 2 PAS (PER-ARNT-SIM) dimerization domains.
 CC -!- SIMILARITY: Contains 3 PAS-associated C-terminal (PAC) domains.
 CC --!- SIMILARITY: Contains 1 EAL domain.
 CC ---!- SIMILARITY: Contains 1 GGDEF domain.

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CC DR EMBL; AE000296; AAC75128.1; -.
 CC DR EMBL; D90844; BA015920.1; -.
 CC DR EMBL; D90845; BA015925.1; -.
 CC DR EMBL; K02488; -; NOT_ANNOTATED_CDS.
 CC DR PIR; B64973; B64973.
 CC DR EcoGene; EG12396.1.
 CC DR InterPro; IPR001633; EAL.
 CC DR InterPro; IPR001610; GGDEF.
 CC DR InterPro; IPR001610; PAC.
 CC DR InterPro; IPR000700; PAS-assoc_C.